```
Matches
                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                          01-MAY-1997
01-MAR-2001
                                                                    01-MAY-1997
                                                                                                                                                                                                                                                                                    Lyase.
SEQUENCE
  Erwinia
                             HRCC PRECURSOR
                                                                                  P94767
                                                                                                                                                                                                                                                                                                                                                   "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
EMBL; AE002054; AAF11756.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                  White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Pet
Dodson R.J., Haft D.H.; Gwinn M.L., Nelson W.C., Richar
Moffat K.S., Qin H., Jiang L., Pemphile W., Crosby M.,
Vamathevan J.J., Lam P., McDonald L., Utterback T., Zal
Makarova K.S., Aravind L., Daly M.J., Minton K.W., Flei
Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Ven
                                                                                               P94767
                                                                                                                                                                                                                                                                                                              Pfam; PF00903;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-R1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Deinococcus radiodurans.
Bacteria; Thermus/Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RSB7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RSB7
                                                                                                                                                                                                                                                                                                                                                                                                           raser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-20036896; PubMed-10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACTOYLGLUTATHIONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hydrolase.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00561; abhydrolase; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the 8 Mb Streptomyces coelicolor A3(2) c
Mol. Microbiol. 21:77-96(1996).
-I- SIMILARITY: TO ALPHA/RETA HYDROLASE
EMBL. AL031155; CAA20070.1;
                                                                                                                                                                                                                                                                                                                              interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                               94
                                                                                                                                                                                         1 ISRFAWGE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ISRFAWGEV 9
                                                                                                                                                              VTRYAWGE 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LTRYAWGEI 369
chrysanthemi
                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                           IPR000325; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR000073; -. IPR000379; -.
                                     (TrEMBLrel.
(TrEMBLrel.
                                                                                                                                                                                                                                                                                    126 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      449 AA;
                                                                                            PRELIMINARY;
                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TremBLrel. 13, Created)
(TremBLrel. 13, Last sequence update)
(TremBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                            Glyoxalase; 1
                                                                                                                                                                                                                                                                                 13727 MW;
                                                                                                                                                                                                                             77.6%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     47531 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81.6%;
55.6%;
                                       03,
16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PUTATIVE
                                                  Last
                                                                 Created)
                                                                                                                                                                                                                             Score 38; 1
Pred. No. 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40; DB
Pred. No. 14;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  group;
                                                                                                                                                                                                                                                                                39623D6AB662A418 CRC64;
                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EC74CB1BF3203927 CRC64;
                                   sequence update)
annotation update)
                                                                                            691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Deinococcales; Deinococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB
14;
                                                                                                                                                                                                                                        DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FOLD.
                                                                                           ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                       Length 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 449;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richardson D.L.,
                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peterson J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Zalewski
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Shen M.,
                                                                                                                                                                                                               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
RESULT
Q91602
ID Q1
AC Q2
DT 0
                                                                        밁
                                                                                           Š
                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SQ PT N
                                                                                                               Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
Q91602
Q91602;
01-NOV-1996
                                                                                                                                                                 PROSITE; PS00
Hypothetical
SEQUENCE 28
                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997
01-FEB-1997
01-JUN-2000
                                                                                                                                                                                                                                                                             MEDLINE=97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S., Kimura T.,
Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.
                                                                                                                                                                                                                                                   "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the
                                                                                                                                                                                                                                                                                                                                                                   Synechocystis sp. (strai
Bacteria; Cyanobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kim J.F., Bauer D.W., Col. Submitted (MAY-1996) to tl EMBL; L39897; AAC31975.1; InterPro; IPR000016; -.
                                                                                                                                                                                                                    EMBL; D90907; BAA17566.1;
                                                                                                                                                                                                                                        entire genome and assignment of
                                                                                                                                                                                                                                                                                                                                                                                                 HYPOTHETICAL
                                                                                                                                                                                                  etam;
                                                                                                                                                                                                                                ONA Res.
                                                                                                                                                                                                                                                                          Pabata S.;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                          P73526;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     P73526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-EC16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR01337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pectobacterium
                                                                                                                                                                                                            nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003522;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 SRFGWGEL 149
                                                                       73
                                                                                           1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 SRFAWGEV 9
                                                                       ISRYAWG
                                                                                                                                                                                                  PF00037;
                                                                                                               Similarity6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
6; Conserv
                                                                                                                                                                                   PS00198; 4FE4S_FERREDOXIN; UNKNOWN_1.
                                                                                                                                                                                                                               3:109-136(1996)
                                                                                                                                                               -ar protein.
289 As-
                                                                                                                                                                                                           IPR001450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  691
                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
(TrEMBLrel.
L 32.6 KDA PR
                    PRELIMINARY;
                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                       79
                                                                                                                                                                                               fer4; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bac_GSPproteins;
7; TYPE3OMGPROT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                  (strain PCC 6803).
cteria; Chroococcales;
                                                                                                                                                                  32551 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31
74829
                                                                                                                        75.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Collmer A.,
                                                                                                                                                                                                                                                                                                                                                                                                          02, Creat
02, Last
14, Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gamma
                                                                                                            Score 37; DB Pred. No. 31; 1; Mismatches
                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 38;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POTENTIAL.
25EC46876959EB2F CRC64;
                                                                                                                                                                DE79651E9AB31DA9 CRC64;
                                                                                                                                                                                                                                        potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                          annotation
                                                                                                                                                                                                                                                                                                                                                                                                                    sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Beer S.V.;
                   394
                                                                                                                                                                                                                                                                                                                                                                                                                                                   289
                                                                                                                         DB
31;
                                                                                                                                                                                                                                                                                                                                                                  Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                       protein-coding
                                                                                                                                   2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2,
                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 databases
                                                                                                                                  Length 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length
                                                                                                              Indels
                                                                                                                                                                                                                                       ination of the ingregions
                                                                                                                                                                                                                                                                               Okumura
asuda M.,
                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

(TrEMBLrel.

```
Query Match
Best Local Similarity
"Arches 5; Conserve
                                                               SULT
U5B4
                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                       Matches
 Q9U5B4
Q9U5B4;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q92J05;
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-2000 (TrEMBLrel. 13,
PROTON-TRANSLOCATING ATPASE
                                                                                                                                                                                                                                                                             "Cloning and Structure/Function Studies of a Proton-Translocating AfPase from the Oral Streptococci Streptococcus sanguis."; Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases. EMBL, AF001955; AAD00914.1; -. InterPro: IRR002146; -. Pfam; pF00430. ~~
                                                                                                                                                                                                                                                          Pfam; PF00430; ATP-synt_B; 1. SEQUENCE 164 AA; 17595 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Firmicutes; Streptococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q92J05
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Streptococcus sanguis
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=1305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001201; -.
InterPro; IPR002934; -.
Pfam; PF01909; NTP_transf_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Cloning and characterization of a Xenopus Mol. Cell. Biol. 15:1422-1430(1995).
EMBL: U23456; AAA64708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gebauer F., Richter J.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=95166227; PubMed=7862135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               376 LAMFAWGEI 384
                                                                                                                          26 IKKFAWGNI 34
                                                                              10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 ISRFAWGEV 9 :: ||||||:
                                                                                                                                                       ISRFAWGEV 9
                                                                                                                                                                                    Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   POLYMERASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        394 AA;
 (TrEMBLrel. 13, (TrEMBLrel. 13,
                                               PRELIMINARY;
                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.5%;
55.6%;
                                                                                                                                                                                                  73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     45326 MW; .74E4684EF3C1B967 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01,
Created)
Last sequence update)
                                                                                                                                                                                Score 36; DB Pred. No. 26; 2; Mismatches
                                                                                                                                                                                    2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ÿ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 37;
Pred. No.
                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                           37ABD5392F6E212D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                            169 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     164 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
43;
                                                                                                                                                                                                                DB
                                                                                                                                                                                                               2; Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Length 394;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            poly(A) polymerase.";
                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
```

```
δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8888
                                                                                                                                                                                                                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RRRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BRISTOL N2;
Gattung S., Du H., Sci
"The sequence of C. e.
Submitted (DEC-1999)
                                                                                                                                                                                                                                                                    Q9Q0E5 PRELIMINARY; PRT;
Q990E5;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sec
01-MAR-2001 (TrEMBLrel. 16, Last and
NONSTRUCTURAL PROTEIN 1 (FRAGMENT).
                                                                 "Molecular characterization of H9N2 influenza viruses: were they the donors of the 'internal' genes of H5N1 viruses in hong kong?"; Proc. Natl. Acad. Sci. U.S.A. 96:9363-9367(1999).
EMBL; AF156484; AAD52959.1; -.
HSSP; P03495; IAIL.
                                     InterPro; IPR000256; -.
Pfam; PF00600; Flu_NS1; 1.
                                                                                                                                             STRAIN=A/QUAIL/ARKANSAS/29209-1/93;
MEDLINE-99362763; PubMed-10430948;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                  Influenza A virus (A/Quail/Arkansas/29209-1/93 (H9N2)).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses; Influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (DEC-1999) to the EMBL; AC017117; AAF16612.1; InterPro; IPR003326; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans.
Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
 SEQUENCE
              NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Genome sequence of the nemainvestigating biology. The C
Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           None;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-2001 (TrEMBLrel. F43C11.2 PROTEIN.
                                                                                                                                                                                                        NCBI_TaxID=97395;
                           Monstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF02343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F43C11.2
                                                                                                                                                                                                                                                                                                                                                                                                                  106 VARYSWGQV 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 44.
                                                                                                                                                                                                                                                                                                                                                                          H
                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ISRFAWGEV 9
 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         169 AA;
 AA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DUF130;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scheet P., Hawrysko C.; elegans cosmid F43C11."; 9) to the EMBL/GenBank/DDBJ
 25806 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19239 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nematoda; Chromadorea; cinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The C. elegans Sequencing Consortium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16,
                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 36; Pred. No.
363D913707208C08 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3E0BF405CFB19505_CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                               228 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rhabditida; Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                     A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
```

Query Match Best Local Similarity

73.5%; 85.7%;

Score Pred.

36; No.

ДВ 37;

14;

Length 228;

```
SOUTH THE TENT OF THE FEET OF 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
MEDLINE AV. Simpson A.J.G., Rein
     MEDLINE-20365717; Pubhed-10910347;
Simpson A.J.G., Reinach F.C., Arru
Alvarenga R., Alves L.M.C., Araya
                                                                                                 STRAIN-9A5C
                                                                                                                                                                                                                                                       Xylella fastidiosa
                                                                                                                                                                            NCBI_TaxID=2371;
                                                                                                                                                                                                            xylella.
                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                      NADH-UBIQUINONE
                                                                                                                                                                                                                                                                                                                                                01-OCT-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9PGJ3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9PGJ3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MO1. Microbiol. 21:77-96(1996).
-i- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.
EMBL; AL079355; CAB45571.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptomyces coelicolor.

Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

Bacteria; Firmicutes; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XAN3;
Q9XAN3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed the 8 Mb Streptomyces coelicolor A3(2) chmol. Microbiol. 21:77-96(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1999 (TremBlrel. 12, Created)
01-NOV-1999 (TremBlrel. 12, Last sequence update)
01-MAR-2001 (TremBlrel. 16, Last annotation update)
PUTATIVE 3-OXOADIPATE ENOL-LACTONE HYDROLASE/4-CARBOXYMUCONOLACTONE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seeger S., Harris D.;
"A set of ordered cosmids and a detailed genetic and physical the 8 Mb Streptomyces coelicolor A3(2) chromosome.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR00111; ABHYDROLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Redenbach M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (JUN-1999)
                                                                                                                   EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       -OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISRYAWGEI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity 7; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IPR003089; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000379;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IPR000073;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 375
                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Parkhill
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kieser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ά,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abhydrolase;
                                                                                                                                                                                                                                                                                                                 OXIDOREDUCTASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              39873 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                91.8%;
77.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         J., Barrell B.G., Rajandream M.A.;
to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Denapaite D.,
                                                                                                                                                                                                                                                                                                                                          Last
                                                                                                                                                                                                                                                                                                                                                                       Last
                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 45; DB
Pred. No. 1.3;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                 NQO5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67176A8F3E61EECC CRC64;
                                                                                                                                                                                                                          subdivision; Xanthomonas
                                                                                                                                                                                                                                                                                                           sequence update)
annotation updat
NQO5 SUBUNIT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
1.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       chromosome.
     Abreu
Baia G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eichner A., Cullum J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ₹
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2
                                                                                                                                                                                                                                                                                                                                     update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 375
                               Acencio M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              physical map
                                                                                                                                                                                                                          group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Qγ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 6; Conser
                                                                                                          SEQUENCE
STRAIN-A3(2);
STRAIN-A3(2);
STRAIN-A3(2);
STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A., de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A., Peixoto B.R., Pereira G.A.G., Pereira H.A. Jr., Pesquero J.B., Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M., de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E., de Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr., da Silveira J.F., Silvestri M.L.Z., Siqueira W.J., de Souza A.A., de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
            Redenbach M.,
Kinashi H., H
                                       MEDLINE-97000351; PubMed-8843436;
                                                           STRAIN-A3(2);
                                                                                                                                                                                 Submitted
                                                                                                                                                                                                  Oliver K.
                                                                                                                                                                                                                                                                                        Streptomyces coelicolor. Bacteria; Firmicutes; Ac
                                                                                                                                                                                                                                                                                                                                              01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
3-OXOADIPATE ENOL-LACTONE HYDROLASE/4-CARBOXYMUCONOLACTONE
                                                                                                       Submitted
                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                            STRAIN-A3(2);
                                                                                                                                                                                                                            SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                   086608;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H. Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L., Zago M.A., Zatz M., Meidanis J., Setubal J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R., Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A., Ho P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P., Krieger J.E., Kuramae E.E., Laigret F., Lambais M.R., Leite L.C.C. Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A., Madeira A.M.B.N., Madeira H.M.F., Marino C.L., Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y., Menck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B., Monon D.H., Nagai M.A., Nascimento A.L.T.O., Netto L.E.S.,
                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                          NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                        Actinomycetales;
                                                                                                                                                                                                                                                                                                                        SC3A7.07
                                                                                                                                                                                                                                                                                                                                                                                                                                809980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00329; complex1_30Kd; 1. PROSITE; PS00542; COMPLEX1_30K; SEQUENCE 250 AA; 28081 MW; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of the plant Nature 406:151-159(2000).
EMBL; AE003884; AAF83118.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fraga J.S., Franca S.C., Franco N
                                                                                                                                                                                                                                                                                                                                     DECARBOXYLASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bueno M.R.P., Camargo A.A., Camargo L
Colauto N.B., Colombo C., Costa F.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Coutinho L.L., Cristofani M., Dias-Neto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90 VGRFAWGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ISRFAWGE 8
                                                                                                      (JUL-1998)
                                                                                                                                                                            (JUL-1998)
                                                                                                                                                                                                                                                                                   Firmicutes; Actinobacteria; Actinobacteridae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IPR001268;
           Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                     Streptomycineae;
                                                                                                    B.G.,
to th
                                                                                                                                                                                 ç
                                                                                                      the
                                                                                                                                                                               the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E.D.,
                                                                                               Rajandream M.A.;
e EMBĻ/GenBank/DDBJ databases
                       Denapaite D.,
                                                                                                                                                                            EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Camargo L.E.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 40;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bordin S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2A96C7D0C981F8DB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    rerreira V.C.A., Ferro J.A.,
                                                                                                                                                                                                                                                                     Streptomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                           449 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Costa M.C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ., Gomes S.L., Gruber A.,
Kemper E.L., Kitajima J.P.,
Lambais M.R., Leite L.C.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BB
                      Eichner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bove J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Xylella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ve J.M., Briones
Carraro D.M., Ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fastidiosa.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.M., Carrer H.,
Costa-Neto C.M.,
                       Cullum J
                                                                                                                                                                                                                                                                  Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       El-Dorry H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       M. K.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0,
```

and

detailed

genetic

and

physical map

```
itle:
erfect score:
equence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         esult.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               atabase : .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           num DB seq length: 0 aximum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Otal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          earched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           coring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : no nu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           M protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Match Length DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-646-579-2
49
1 ISRFAWGEV 9
1: sp_archea:*
2: sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 18, 2001, 16:53:10; Search time 33.31 Seconds (without alignments) 35.747 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPTREMBL_16:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp_rodent: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sp_plant:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        _human:*
126
691
289
394
164
169
228
228
229
223
230
230
230
230
                                                Q9XD79
Q9XAN3
Q9PGJ3
Q9PGJ3
Q9RSB7
P94767
P73526
Q91602
Q925B4
Q90025
Q9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              425026
                                                                                                                                                                                                                                P73526 synechocyst
Q91602 xenopus lae
Q9zj05 streptococc
Q9u5b4 caenorhabdi
                                                                                                                                                                                                                                                                                                                                                Q9xd79 streptomyce
Q9xan3 streptomyce
Q9pgj3 xylella fas
086600 streptomyce
Q9rsb7 deinococcus
P94767 erwihia chr
                                                                                              0990e5 influenza a
0990e3 influenza a
041651 influenza a
041653 influenza a
041654 influenza a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Description
```

45	44	3	42	4	40	39	38	37	36	35	34	ω ω	32	ω μ	30	29	28	27	26	25	24	23	22	21	20
36	36	36	36	3 6	36	36	36	36	36	36	36	36	36	36	36	36	36 .	36	36	36	36	36	36	36	36
73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5		73.5	73.5		73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5	73.5		73.5	73.5
451	272	230	230	230	230	230.	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230	230
G	N	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14
Q9TXV7	054375	Q9DGY0	Q9EA66	Q9EA72	Q9Q0L6	Q9WC10	Q9WC12	Q9WC13	Q9WC14	Q9WC15	Q9WC16	Q9WC18	Q9WC19	Q9WC20	089283	Q82813	092785	092650	092649	Q82804	009704	009702	Q04262	042082	042067
Q9txv7	054375	Q9dg:	Q9ea66	Q9ea72	099016	Q9wc10	Q9wc12	Q9wc13	.09wc14	< 09wc15	Q9wc16	Q9wc18	Q9wc19	Q9wc20	089283	. Q82813	092785	092650	092649	Q82804	009704	009702	Q04262	042082	04206
7 c:	5									-			-	_		Ċ		50						N	7
caenorhabdi	S			influenza a																	influenza a				influenza a
		_		_		_				₩.				<u>u</u>		٠ س	٠ س					w		_	

ALIGNMENTS

D Qy	Quer Best Matcl			 및 및			Υ Ά						۶ ۲					ğ			Q9XD79	
1 ISREAWGEV 9 : : 288 ISRYAWGEI 296	SEQUENCE 373 AA; 39583 MW; F11D3017D7A524DC CRC64; Query Match 91.8%; Score 45; DB 2; Length 373; Best Local Similarity 77.8%; Pred. No. 1.3; Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;	© 373 33. 20502 M. 111720117117101	Pfam; PF00561; abhydrolase; 1. PRINTS; PR00111; ABHYDROLASE	InterPro; IPR000073;	EMBL; AF109386; AAD40815.1;	-!- SIMILARITY: TO ALPHA/BETA HYDROLASE FOLD.	/MAV-1000) to the EWEI /Company /Dept databases	ocatechuate cataboli	Yang K., Iwaqami S., Davies J.E.:	STRAIN=2065	SEQUENCE FROM N.A.	[1]	ACCINOMYCETALES; Streptomycineae; Streptomycetaceae; Streptomyces. NCBI TaxID=86383:	Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;	Streptomyces sp. 2065.	PCAL.	CONOLACTONE DECARBOXY	01-MAR-2001 (TrEMBLiel. 16. Last sequence update)	(Tremburel, 12,	Q9XD79 PRELIMINARY; PRT; 373 AA.		F

RESULT

```
AC POSOSS;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE MYELIN BASIC PROTEIN (MBP).

MEDLINED ANSIC PROTEIN (MBP).

OC MARD (MBP).

OC MARD (MBP).

OC MARD (MBP).

RAP (MBP).

OC MARD (MBP).

RELIMINARY SEQUENCE.
RELIMINARY SEQUENCE of the encephalitogenic protein from richimpanzee brain.*
RELIMINARY SEQUENCE.
RELIMINARY SEQUENCE.
RELIMINARY SEQUENCE.
RELIMINARY SEQUENCE.
RELIMINARY RELIMINARY FUNCTION TO MAINTAIN PROPER STRUCTURE
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.
CC -1- SUBCELLULAR BECOMES TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SIMILARITY BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELLULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELULAR BROOSS TO THE MYELIN BASIC PROTEIN FAMILY.
CC -1- SUBCELULAR BROOSS TO THE MYELI
```

Search completed: October 18, 2001, 16:52:30 Job time: 115 sec

```
(ESULT 14

MBP_BOVIN

D MBP_BO
                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Thehes 5; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             eeees
                                                                                                 Query Match
Best Local
                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAVPO
MBP_CAVPO
 MBP_BOVIN
                                                                                                                                      SEQUENCE
                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                 Shapira R., McKneally S.S., Chou F., Kibler R.F.; "Encephalitogenic fragment of myelin basic protein. Sequence of bovine, rabbit, guinea pig, monkey, and J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                   MEDILINE-84215086; PubMed-6202840;
Deibler G.E., Martenson R.E., Krutzsch H.C., Kies M.W.;
"Sequence of guinea pig myelin basic protein.";
J. Neurochem. 43:100-105(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eut
Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1992 (Rel. 22, Crea
01-MAY-1992 (Rel. 22, Last
30-MAY-2000 (Rel. 39, Last
MYELIN BASIC PROTEIN (MBP)
                                                                                                                                                                           MOD_RES
                                                                                                                                                                                                                           PRINTS;
                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF -1- SIMILARITY: BELONGS TO THE MYELIN BASIC PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Cavia porcellus (Guinea pig).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INIT_MET
MOD_RES
MOD_RES
                                                                                                                                                                                            Autoimmune encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P25188;
                                                 110
                                                                                                                                                                                                        (yelin;
                                                                                                                                                                                                                                            InterPro; IPR000548; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                     EQUENCE OF 45-87.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 LSRFSWG 114
                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE.
                                                                   1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ISRFAWG 7
                                                :|||:||
LSRFSWG
                                                                                                                                                                                                                                                                                              OF MYELIN
                                                                                                                                                                                                                                                     C92087; C92087.
                                                                                                                                                                                                                                                               A37246; A37246.
                                                                                                                                                                                                                                  PF01669; Myelin_MBP; 1.
                                                                                     Similarity
5; Conserv
                                                                                                                                                                                                      Structural protein; A
                                                                                                                                    167
                                                                                      Conservative
                                                                                                                                                         114
                                                                                                                                                                           106
                                                116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                    AA;
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                         MYELINMBP
                                                                                                                                                                          106
                                                                                                                                                        122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   104
104
47
124
                                                                                                                                   18213 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                   Score 35;
Pred. No.
2; Mismato
                                                                                                                                                                                                    Acetylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2:
                                                                                                                                   ENCEPHALOMYELITIS.
866D31F1E5ACFEA6
                                                                                                                                                    INDUCES EXPERIMENTAL AUTOIMMUNE
                                                                                                                                                                 METHYLATION (MONO-
SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 35;
Pred. No.
                                                                                                                                                                                  ACETYLATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  METHYLATION (MONO-:44% OR DI-:11%).
SG -> GS (IN REF. 4).
M -> I (IN REF. 2).
 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACETYLATION.
                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3 -> GS (IN REF. 4).
-> I (IN REF. 2).
B4C9F33C19A9E137 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              on update)
169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     167
                                                                                                ထ
                                                                                              .5
BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB
Ā
                                                                                                                                                                                                  Methylation; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A
                                                                                                      ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                      PROTEIN FAMILY
                                                                                    0;
                                                                                                                                                                                                                                                                                MYELIN
                                                                                                     Length 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                   CRC64;
                                                                                                                                                                        OR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 127
                                                                                                                                                                        DI-) (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                               Amino
                                                                                                                                                                                                                                                                                                                       human
                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                              acid
                                                                                                                                                                                                                                                                                                                     fragments.";
                                                                                                                                                                                                                                                                                                  STRUCTURE
                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
Query Match
Best Local Similarity
---hes 5; Conserv:
    밁
                                      δÃ
                                                                                                                                                                                               SOFT THE WAR BORRES COCCORDED TO THE WAR BORRES COCCORDED 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RRN OCC OCC DE DE
                                                                                                                                                                                                                                     MOD_RES
MOD_RES
DOMAIN
                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDITARY 1103946; PubMed-4994464;

Brostoff S.W., Eylar E.H.;

"Localization of methylated arginine in the Al protein from proc. Natl. Acad. Sci. U.S.A. 68:765-769(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P02687;
21-JUL-1986
21-JUL-1986
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01669; Myelin_MBP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SUBCELLULAR LOCATION:
-!- SIMILARITY: BELONGS TO
PIR; A03140; MBBOB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Brostoff S.W., Reuter W., Hichens M., "Specific cleavage of the A1 protein J. Blol. Chem. 249:559-567(1974).
                                                                                                                                                                                                                                                                                                  Autoimmune encephalomyelitis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eylar E.H., Caccam J., Jackson J.J., Westall F.C., "Experimental allergic encephalomyelitis: synthesi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SYNTHESIS OF ALLERGIC ENCEPHALOMYELITIS INDUCING MEDLINE-70178977; PubMed-5442707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shapira R., McKneally S.S., Chou F., Kibler R.F.; "Encephalitogenic fragment of myelin basic protein sequence of bovine, rabbit, guinea pig, monkey, and J. Biol. Chem. 246:4630-4640(1971).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
:|||:||
110 LSRFSWG
                                                                                                                                                                                                                                                                                                                           Myelin;
                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -!- FUNCTION: THIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disease-inducing site of the basic Science 168:1220-1223(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    METHYLATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 43-87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=74070688; PubMed=4129204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=72007306; PubMed=5096093;
Eylar E.H., Brostoff S.W., Hashim G., Cac
"Basic Al protein of the myelin membrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REVISION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MYELIN
                                        1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OF MYELIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BASIC
                                                                                                                                                                                                                                                                                                                        Structural
                                                                                                                                                                                                                                                                                                                                                                 PR00212; MYELINMBP
                                                                                                                                                                                                                                                                                                                                             PS00569; MYELIN_MBP;
                                                                                                                                                                                          169 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Bovine)
                                                                                                                                                                                                                                       106
114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel.
(Rel.
                                                                                     Conservative
  116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    246:5770-5784(1971)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01, Last sequence update)
39, Last annotation update)
EIN (MBP) (MYELIN Al PROTEIN).
                                                                                                                                                                                                                                          \frac{106}{122}
                                                                                                                                                                                                                                                                                                                           protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROTEIN
                                                                                                                                                                                             18323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chordata; Craniata; Vertebrata;
Cetartiodactyla; Ruminantia; Pe
                                                                                                       71.48;
                                                                                                                           71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                      ТО
                                                                                                                                                                                          ₩,
                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYTOPLASMIC SIDE OF MYELIN.
O THE MYELIN BASIC PROTEIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAY FUNCTION TO MAINTAIN PROPER
                                                                                   2;
                                                                                                                                                                                                                                                                                                                      Acetylation;
                                                                                                                                                                                 ACETYLATION (MONO- OR DI-).
METHYLATION (MONO- OR DI-).
INDUCES EXPERIMENTAL AUTOIMMUNE
ENCEPHALOMYELITIS;
8E1157B7A1978484 CRC64;
                                                                                                   Score 35; I
                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eylar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caccam J.,
                                                                                                   B.6;
                                                                                                                                                                                                                                                                                                                      Methylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ar E.H.;
myelin with cathepsin D.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The
                                                                                                                         ۲.
                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complete
                                                                                                                       Length 169;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burnett P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pecora;
                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Robinson
s of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            human fragments.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Euteleostomi;
                                                                                                                                                                                                                                                                                                                  Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bovoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE
                                                                              0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              myelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acid
                                                                            0
```

RESULT 15
MBP_PANTR
ID MBP_PANTR

STANDARD;

PRT;

171 AA

restrictions

in

no 9

Way

밁 δã

```
TOCOCORRER RANGOCOS SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           유
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SE DE DE COCOCO
 Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                     Flagella.
SEQUENCE
                                                                                                                      PIR;
                                                                                                                                   EMBL; M87526; AAA33092.1;
                                                                                                                                                                    or send an email to license@isb-sib.ch)
                                                                                                                                                                                       entities
                                                                                                                                                                                                                                        the
                                                                                                                                                                                                                                                         between
                                                                                                                                                                                                                                                                         This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Curry A.M., Williams B.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-GCT-1993 (Rel. 27, Last annotation update)
FLAGELLAR RADIAL SPOKE PROTEIN 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence analysis reveals homology between two proteins of the flagellar radial spoke."; Mol. Cell. Biol. 12:3967–3977(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chlamydomonas reinhardtii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro: IPR000256; -.
Pfam; PF00600; Flu_NSI; 1.
NONSTRUCTURAL PROTECTION: Alternative splicing.
SEQUENCE 230 AA; 26076 MW; 3FDEZ73901ED1D7C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=92375065; PubMed=1508197;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RSP4_CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M55466; AAA43132.1; HSSP; P03495; IAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (S or send an email to license@isb~sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              201656;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198
                                                                                                                                                                                                                                                                                            OF THE OUTER DOUBLET MICROTUBULE, AND A BULBOUS HEAD, WHI ATTACHED TO THE STALK AND APPEARS TO INTERACT WITH THE PROJECTIONS FROM THE CENTRAL PAIR OF MICROTUBULES.
SUBUNIT: THE RADIAL SPOKE HEAD IS MADE OF FIVE DIFFERENT POLYPEPTIDES (RSP1, RSP4, RSP6, RSP9, AND RSP10).
SUBCELLULAR LOCATION: RADIAL SPOKE.
SIMILARITY: TO THE FLAGELLAR RADIAL SPOKE PROTEIN 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ISRFAWG
                                                                                                                                                                                                                  European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                FUNCTION: FLAGELLAR RADIAL SPOKES CONTRIBUTE TO THE REGULATION OF DYNEIN ARM ACTIVITY AND THUS THE PATTERN OF FLAGELLAR BENDING. THEY CONSIST OF A THIN STALK, WHICH IS ATTACHED TO THE A SUBFIBER
                                                                                                                      A44498; A44498
                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IQRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 6; Conser
                                                                                                                                                                                  and this statement is not removed. requires a license agreement (See
                                                                                     465 AA;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                     49798
                 73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.5%;
85.7%;
                                                                                     ₹:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rosenbaum J.L.;
   0,
                 Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; Pred..No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                 A23AFB030CDB3E29
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            465
                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              moved. Usage by and for commercial (See http://www.isb-sib.ch/announce)
                                                                                                                                                                                                                                 There are no
                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1;
                                                                                                                                                                                                                   as its content
                                                                                                                                                                                                Usage
0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1;
                                Length 465;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 230
                                                                                   CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                  ЬY
                                                                                                                                                                                                                               restrictions
                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and
                                                                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                      WHICH
                                                                                                                                                                                                                     ŝ
                                                                                                                                                                                                                                                                  a collaboration
                                                                                                                                                                                                  for
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for commercial
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                  commercia.
                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

Myélin; Structural protein;

encephalomyelitis; Alternative splicing

Acetylation; Methylation; Phosphorylation;

PS00569; MYELIN_MBP; 1

PROSITE;

```
MBP_RAT
ID MBF
AC P02
DT 21-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JUL-1986
21-JUL-1986
30-MAY-2000
                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                  EMBL; M25889; AAA41575.1;
EMBL; K00512; -; NOT_ANNO
                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=73180720; PubMed=4122324; McFarlin D.E., Blank S.E., Kibler R.F., McKneally S., "Experimental allergic encephalomyelitis in the rat: necephalitogenic proteins and peptides."; Science 179:478-480(1973).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=84026484: PubMed=6194889;
Roach A., Boylan K., Horvath S., Prusiner S.B., Hood L.E.;
Roach A., Boylan K., Horvath S., Prusiner S.B., Hood L.E.;
"Characterization of cloned cDNA representing rat myelin basic
protein: absence of expression in brain of shiverer mutant mice.";
C211 34:799-806(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MBP_RAT
P02688;
Pfam; PF01669; Myelin_MBP;
PRINTS; PR00212; MYELINMBP
                                                                         PIR; B24351; B24351.
PIR; A21062; A21062.
                                                                                                                          PIR; A03142; MBRTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Amino acid sequence of the smaller basic protein from rat brain myelin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Cloned proteolipid protein and myelin basic protein Transcription of the two genes during myelination."; Biol. Chem. Hoppe-Seyler 367:825-834(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                              between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of MYELIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dunkley P.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-87026249; PubMed-2429678; Schaich M., Budzinski R.M., Stoffel W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 45-85.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Biochem. J. 141:243-255(1974).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=75127359; PubMed=4141893;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MYELIN BASIC
                                                    nterPro; IPR000548; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          438 FAWGEV 443
                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: CYTOPLASMIC SIDE OF MYELIN.

ALTERNATIVE PRODUCTS: RATS HAVE TWO MYELIN BASIC PROTEINS. THE
SMALLER ONE, SHOWN HERE, IS MISSING 40 RESIDUES (FOLLOWING RESI
113 OR 114) WITH RESPECT TO THE LARGER ONES FROM OTHER SPECIES.

SIMILARITY: BELONGS TO THE MYELIN BASIC PROTEIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 FAWGEV
                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the Ew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 01, Created)
(Rel. 01, Last seq
(Rel. 39, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               THIS PROTEIN MAY FUNCTION TO MAINTAIN PROPER STRUCTURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Carnegie P.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                               NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Chordata;
Rodentia;

    Last sequence update)
    Last annotation update)
    S (MBP S)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Craniata; Veri
Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127
                                                                                                                                                                                                                                                                                                                    There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vertebrata; Euteleostomi;
thi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        response
                                                                                                                                                                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                      a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESIDUE
```

```
CCPRRRRRRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ĉ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Matci
Best Local
                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 rtches
                                                                                                                        EMBL; M55467; AAA43124.1; -.
HSSP; P03495; 1AIL.
InterPro; IPR000256; -.
Pfam; PF00600; F1L_MS1; 1.
Nonstructural protein; Alternative splicing.
SEQUENCE 230 AA; 26174 MW; 3FDE27220050701C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P30910;
01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last sequence update)
01-JUL-1993 (Rel. 26, Last annotation update)
                                                                                                                                                                                                                         entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in most by non-broken used this statement is not removed. Usage by and for competitive
                                                                                                                                                                                                                                                                                                                                                                      influenza A viruses.";
Virology 183:566-577(1991).
                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-91306439; PubMed-1830182;
Eudwig S., Schultz U., Mandler J., Fitch W.M., Scholtissek C.;
"Phylogenetic relationship of the nonstructural (NS) genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between the Swiss Institute of Bioinformatics and the European Bioinformatics Institute. There are no use by non-profit institutions as iong as its conmodified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or.send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                      between
                                                                                                                                                                                                                                                                                                                    This
                                                                                                                                                                                                                                                                                                                                                               -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Turkey/Bethlehem-Glilit/1492-B/82).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NONSTRUCTURAL PROTEIN NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IATKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000256; -.
Pfam; PF00600; Flu_NS1; 1.
Nonstructural protein; Alternative splicing.
SEQUENCE 230 AA; 26071 MW; D738A943C8FFBC84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; G32663; MNIVA8.
HSSP; P03495; IAIL.
InterPro; IPR000256;
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M25370;
198 IQRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS1_IATKB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
les 6; Conser
                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                        ALTERNATIVE PRODUCTS: NS1 AND NS2 PROTEINS ARE PRODUCED ALTERNATIVE SPLICING OF SEGMENT 8.
                       ISRFAWG
                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IQRFAWG
                                                         Similarity 6; Conserv
 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAA43559.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                     73.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.5%;
                                                     Score 36; DB:
Pred. No. 7.5;
0; Mismatches
                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36; DB .Pred. No. 7.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB
7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Å
                                                                                1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                      1;
                                                                                Length 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and the
                                                      Indels ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        restrictions on
                                                                                                                                                                                                                                                                                                   EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL outstation
                                                                                                                                                                                                                                                                                                            a collaboration
                                                     0;
                                                                                                                                                                                                                                                                                                                                                         ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                               outstation
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     its
                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

```
TID ACCOUNT OF THE PROPERTY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 9
VNS1_IATKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNS1_IATRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
01-JUL-1993 (Rel. 2
                                                             Virology 183:566-577(1991).
-!- ALTERNATIVE PRODUCTS: NS1 AND NS2
ALTERNATIVE SPLICING OF SEGMENT 8.
                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE=91306439; PubMed=1830182;
Ludwig S., Schultz U., Mandler J., Fitch
"Phylogenetic relationship of the nonstru
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNS1_IATRT P30912;
This SWISS-PROT entry is copyright. between the Swiss Institute of Bioi
                                                                                                                                                                                                                                                                                              Viruses; ssRNA negative-strand
Influenza virus A and B group;
Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-1993 (Rel. 26, Created)
01-JUL-1993 (Rel. 26, Last seq
01-JUL-1993 (Rel. 26, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000256; -.
Pfam; PF00600; Flu_NS1; 1.
Nonstructural protein; Alternative splicing.
SEQUENCE 230 AA; 25964 MW; 41BBA9C6632C1057 CRC64;
                                                                                                                                                                                                                                                                         NCBI_TaxID=11477;
                                                                                                                                                                                                                                                                                                                                                                Influenza A virus (strain A/Tern/Turkmenia/18/72)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         influenza A viruses.";
Virology 183:566-577(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Influenza A virus (strain A/Turkey/Canada/63).
Viruses; ssrNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
NCBI_TaxID=31664;
                                                                                                                                      influenza A viruses."
                                                                                                                                                                                                                                                                                                                                                                                          01-JUL-1993 (Rel. 26, Last annotation NONSTRUCTURAL PROTEIN NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; M55468; AAA43138.1; -. HSSP; P03495; 1AIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=91306439; PubMed=1830182;
Ludwig S., Schultz U., Mandler J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P30911;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NONSTRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Phylogenetic relationship of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNS1_IATKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: NS1 AND NS ALTERNATIVE SPLICING OF SEGMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IQRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROTEIN NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26,26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              . 7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS1 AND NS2
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 36; DB Pred. No. 7.5; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                   viruses; Orthomyxoviridae;
Influenza A viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J., Fitch W.M., the nonstructural
                                                                                                                                                        nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230
                                                                                      PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DВ
7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 There are no restrictions
                                                                                                                                                                                W. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1;
                                                                                      ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           its content
                                                                                                                                                      Scholtissek C.;
l (NS) genes of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scholtissek
l (NS) genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

pht. It is produced through a collaboration
Bioinformatics and the EMBL outstation -

EMBL outstation

```
Query Match
Best Local Similarity
"""+"hes 6; Conserv:
ESULT 6
                                                                                                                                                                   化定换换换换换
                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNS1_IAMA6
P13137;
01-JAN-1990
                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                 EMBL; M25373; AAA43531.1;
PIR; A32663; MNIVA5.
HSSP; P03495; 1AIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                     Treamor J.J., Snyder M.H., London W.T., Murphy B.R.;
"The B allele of the NS gene of avian influenza viruses, but not the A allele, attenuates a human influenza A virus for squirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-1991 (Rel.
01-MAY-1992 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000256; -.
InterPro; IPR000256; -.
Pfam; PF00600; Flu_NS1; 1.
Nonstructural protein; Alternative splicing.
SEQUENCE 230 AA; 26049 MW; DE875F03C8F08FB8 CRC64;
                                                                                                                                                            Pfam; PF00600; Flu_NS1; 1.
Nonstructural protein; Alternative splicing.
SEQUENCE 230 AA; 26021 MW; 39BC9521FAFA9590 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                  198
                                                                                                                                                                                                      InterPro; IPR000256;
                                                                                                                                                                                                                                                                                                                                                                                       ÷
                                                                                                                                                                                                                                                                                                                                                                                                  Virology 171:1-9(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89299445; PubMed=2525836;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Influenza A virus (strain A/Mallard/Alberta/88/76).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NONȘTRUCTURAL PROTEIN NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IAMA6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A04092; MNIV16.
PIR; C32663; MNIVA6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J02105; AAA43509.1;
EMBL; M25372; AAA43529.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  198
                                                                                                               Local Similarity
                                                                           ب
             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                    ALTERNATIVE PRODUCTS: NS1 AND NS2 PROTEINS ARE PRODUCED ALTERNATIVE SPLICING OF SEGMENT 8.
                                                                           ISRFAWG 7
                                                  IQRFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IORFAWG
                                                                                                                                                                                                                                                                  equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 13, Created)
(Rel. 18, Last sequence (Rel. 22, Last anno
                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                             73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
                                                                                                                                                                                                                                            .'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . .
                                                                                                 0;
                                                                                                            Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; I
Pred. No. 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                230
                                                                                                                                                                                                                                                                              (See http://www.isb-sib.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                             DB 1;
7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB
7.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                        Length 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 230,
                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                   restrictions
                                                                                                                                                                                                                                                                                                                               EMBL C
                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                        collaboration
                                                                                                                                                                                                                                                                                                                               outstation
                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                       on
                                                                                                                                                                                                                                                                                                                 on
                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
VNS1_
                                                                                                                                                                                                                                                                                                                                       В
                                                                                                                                                                                                                                                                                                                                                             ş
                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Whiches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                VNS1_IAPI3
P13143;
01-JAN-1990
                                                                 Treanor J.J., Snyder M.H., London W.T., Murphy B.R.:
"The B allele of the NS gene of avian influenza viruses, bu
A allele, attenuates a human influenza A virus for squirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P03495; ....
InterPro; IPR000256; -.
Pfam; PF00600; Flu.NS1; 1.
Nonstructural protein; Alternative
Nonstructural AAA; 26120 MW; C938
                                                                                                       SEQUENCE FROM N.A. MEDLINE-89299445; PubMed-2525836;
                 Virology 171:1-9(1989).
-i- ALTERNATIVE PRODUCTS: NS1 AND NS
ALTERNATIVE SPLICING OF SEGMENT
                                                                                                                                                                 Influenza A virus (strain A/Pintail/Alberta/358/79)
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                    01-JAN-1990 (Rel. 13, Created)
01-MAY-1991 (Rel. 18, Last sequence update)
01-MAY-1992 (Rel. 22, Last annotation update)
                                                                                                                                                                                                                                                                                      IAPI3
                                                            monkeys."
                                                                                                                                                NCBI_TaxID=11452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; M25371; AAA43561.1; -. PIR; E32663; MNIVA7. HSSP; P03495; 1AIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE-89299445; PubMed-2525836;
                                                                                                                                                                                                             NONSTRUCTURAL PROTEIN NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 171:1-9(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A allele,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Treanor J.J., Snyder The B allele of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza virus A and B group; Influenza A viruses; Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-1991
01-MAY-1992
                                                                                                                                                           nfluenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             monkeys.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=11450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; ssRNA negative-strand
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Influenza A virus (strain A/Pintail/Alberta/121/79)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNS1_IAPI1
                                                                                                                                                                                                                                                                                                                                       198 IQRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NONSTRUCTURAL
                                                                                                                                                                                                                                                                                                                                                             1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALTERNATIVE PRODUCTS:
ALTERNATIVE SPLICING C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the En
European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       attenuates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Rel. 13, Created)
(Rel. 18, Last seq.
(Rel. 22, Last anno
                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                     204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rel. 22, Last annotation PROTEIN NS1.
                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                73.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M.H., London W.T., Murphy B.R.;
NS gene of avian influenza viru
a human influenza A virus for s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     : NS1 AND NS2 PROTEINS ARE PRODUCED OF SEGMENT 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             London W.T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence
                                                                                                                                                                                                                                                                                                                                                                                   Score 36; DB
Pred. No. 7.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                cive splicing.
C938C48FB1ED1BCA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    viruses; Orthomyxoviridae;
                                  NS2
                      œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                        230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             230
                                PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                       A
                                                                                                                                                                                                                                                                                                                                                                                                  Ġ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Usage
                                ARE
                                                                                                                                                                                                                                                                                                                                                                                                            Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for squirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                viruses: but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 no restrictions
                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and
                                                                             but not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ВΥ
                                                                                                                                                                                                                                                                                                                                                                                   0,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               outstation
                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           commercia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 its
                                                                                                                                                                                                                                                                                                                                                                                   ç
```

This SWISS-PROT entry

is copyright.

Ħ

is

produced

through a collaboration

```
に作作が何らむこくNPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                        VNS1_IACKG STANDARD;
P30909;
01-JUL-1993 (Rel. 26, Create
01-JUL-1993 (Rel. 26, Last s
01-JUL-1993 (Rel. 26, Last a
NONSTRUCTURAL PROTEIN NS1
                                                                                                                                                                                                                                                                                                                                    ery Match
                MEDLINE=91306439; PubMed=1830182;
                                SEQUENCE FROM N.A.
                                                                   Influenza A virus (strain A/Chicken/Germany/n/49).
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses;
Influenza A virus.
                                                                                                                                                                                                           T 3
                                                                                                                                                                                                                                                                                                                                                                                         NON_TER
                                                           NCBI_TaxID=11339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; provess; NTP transf_2; 1.
Pfam; PF01909; NTP transferase; Transcription;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                    376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U19975; AAC59747.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96079940; PubMed=7489490;
Ballantyne S., Bilger A., Astrom J., Virtanen A., Wickens M.;
"Poly (A) polymerases in the nucleus and cytoplasm of frog occy
dynamic Changes during occyte maturation and early development.
RNA 1:64-78(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADENYLYLTRANSFERASE) (FRAGMENT).
Xenopus laevis (African clawed frog).
Xenopus laevis (African clawed frog).
Zenkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last annotation update)
POLY(A) POLYMERASE TYPE 3 (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                           1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (NUCLEOTIDE) (M+N).
SUBUNIT: MONOMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: POLYMERASE THAT CREATES THE 3' POLY(A) TAIL OF MRNA'S MAY ACQUIRE SPECIFICITY THROUGH INTERACTION WITH A CLEAVAGE AND POLYADENYLATION FACTOR (CPSF).

CATALYTIC ACTIVITY: N ATP + (NUCLEOTIDE)(M) = N PYROPHOSPHATE +
                                                                                                                                                                                                                                                                 LAMFAWGEI 384
                                                                                                                                                                                                                                                                                                                     Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          pean Bloinformatics Institute. There are no rest
non-profit institutions as long as its content
and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               requires a license agreement
     Schultz U.,
                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        400
                                                                                                                                                                                                                                                                                                                                                                                                                                            112
164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                       26, Created)
26, Last sequ
26, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                110
112
164
390
                                                                                                                                                                                                                                                                                                                                                                                                      400
                                                                                                                                                                                                                                                                                                                                                                                       46020 MW;
                                                                                                                                                                                                                                                                                                                               75.5%;
55:6%;
                                                                                                                                      Last annotation
                                                                                                                                                    Last sequence
    Mandler J.,
                                                                                                                                                                                                                                                                                                                                                                                                          BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
NUCLEAR LOCALIZATION S
SIMILARITY).
                                                                                                                                                                                                                                                                                                                    Ψ
                                                                                                                                                                                                                                                                                                                               Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                    AB4347C074E60CA3 CRC64
                                                                                                                                                                                                                                                                                                                   Mismatches
 Fitch W.M.,
                                                                                                                                      on update)
                                                                                                                                                                                            230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                 8.4;
                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RNA-binding
                                                                                                                                                                                                                                                                                                                   1;
Scholtissek
                                                                                                                                                                                                                                                                                                                                            Length 400;
                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                          (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oocytes:
                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ior
                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                                                                                                                                                                                              0
```

```
g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VNS1_IADA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REAL COLOR C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                       STRAIN-A/WALLARD/ALBERTA/827/78;
MEDLINE-8929445; PubMed-2525836;
Treanor J.J., Snyder M.H., London W.T., Murphy B.R.;
"The B allele of the NS gene of avian influenza viruses,
A allele, attenuates a human influenza A virus for squir.
                                                                                                                                                                                             Virology 171:1-9(1989).
-!- ALTERNATIVE PRODUCTS:
ALTERNATIVE SPLICING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-81276929; PubMed-6927848;
Baez M., Zazra J.J., Elliott R.M., Young J.F., Palese P.;
"Nucleotide sequence of the influenza A/duck/Alberta/60/76 virus
"RNA: conservation of the NSI/NS2 overlapping gene structure in a
divergent influenza virus RNA segment.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza A virus (strain A/Duck/Alberta/60/76), and Influenza A virus (strain A/Mallard/Alberta/827/78). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses;
                                                                                                                                                                                                                                                                                  monkeys.
                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-A/DUCK/ALBERTA/60/76;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P03501; P13136;
21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence up
01-MAY-1992 (Rel. 22, Last annotation
NONSTRUCTURAL PROTEIN NS1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Virology 113:397-402(1981).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a chetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=11347, 11432;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Influenza virus A and B group; Influenza Influenza A virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00600; Flu_NS1; 1.
Nonstructural protein; Alternative splicing.
SEQUENCE 230 AA; 26019 MW; 60C643247F62143F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (S or send an email to license@isb-sib,ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNS1_IADA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; M55464; AAA43121.1; HSSP; P03495; LAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Virology 183:566-577(1991).
-i- ALTERNATIVE PRODUCTS: NS1 AND NS2
ALTERNATIVE SPLICING OF SEGMENT 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Phylogenetic relationship influenza A viruses.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR000256; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.5%;
85.7%;
                                                                                                                                                                                               : NS1 AND NS2 PROTEINS ARE PRODUCED OF SEGMENT 8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 36; DB 1
Pred. No. 7.5;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS ARE PRODUCED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                               squirrel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                     but not
                                                                                                                                                                                                                  ВУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in
                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
```

This SWISS:PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).

There are no restrictions ing as its content is in

for

n no way

a collaboration -

outstation

9

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 sum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Potal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mum DB seq length: 0 ...mum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                    %
Query
Match
                                                                                                                                                                                                                                                                               93435 seqs, 34255486 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    October 18, 2001, 16:52:30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-646-579-2
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
 MBP_HUMAN
PA2C. HUMAN
YEGE HAEIN
VNS1_IAAIC
VNS1_IAAIC
VNS1_IAUDO
NU5M_LATCH
NU5M_LATCH
PYG2_SYNEEL
PYG2_SYNEEL
PYG2_SYNEEL
ONAA_STRPN
DNAA_STRPN
DNAA_STRPN
DNAA_STRPN
DNAA_BUGAI
NU5M_CRABI
NU5M_CRABI
NU5M_CRABI
NU5M_CROIA
                                                                                                                                                                                                                                                                                                     VNS1_IATKB
VNS1_IATKC
VNS1_IATRT
                                                                                                                                                                                                                                                                                                                                             PAP3_XENLA
VNS1_IACKG
VNS1_IADA2
VNS1_IAMA6
VNS1_IAPI1
VNS1_IAPI3
                                                                                                                                                                                                                           MBP_PANTR
                                                                                                                                                                                                                                                     MBP_CAVPO
                                                                                                                                                                                                               MBP_MOUSE
                                                                                                                                                                                                                                                                                            RSP4_CHLRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search time 12.81 Seconds (without alignments)
24.067 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                           P30909 influenza a
P03501 influenza a
P13137 influenza a
P13141 influenza a
P13143 influenza a
P13143 influenza a
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                                                          P20370 acinetobact
                     0 synechococc
5 rhizobium s
7 streptococc
8 buchnera ap
2 xenopus lae
8 carassius a
                                                                                                                                          B sus scrofa

mus musculu

homo sapien

homo sapien

haemophilus

influenza a

influenza a
                                                                                                                                                                                                                        pan
sus
cyprinus ca
                                                                                                      caenorhabd1
                                                                                                                   influenza a
latimeria c
                                                                                                                                                                                                                                                 cavia porce
                                                                                                                                                                                                                                                                             rattus norv
                                                                                                                                                                                                                                                                                         chlamydomon
                                                                                                                                                                                                                                                                                                       influenza a
                                                                                                                                                                                                                                                                                                                  influenza a
                                                                                                                                                                                                                                        troglod
```

RESULT 2
PAP3_XENLA
ID PAP3_X
AC P51006
DT 01-OCT

PAP3_XENLA STANDARD; P51006; 01-OCT-1996 (Rel. 34, Created)

PRT;

400 AA.

밁 δÃ

1 ISRFAWGEV 9
|||||||||
41 ISRFAWGEV 49

Query Match
Best Local Similarity
Matches 9; Conser

Conservative

100.0%; Score 49; DB 1; 100.0%; Pred. No. 0.018; Live 0; Mismatches (

0;

0;

Gaps

Length 134; Indels

							•
SQ KW	88888888	488888	R R R R R R R R R R R R R R R R R R R	2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	GE DA DA	RESULT DC4C_A DD D	
EMBL; L0 PIR; B35 Aromatic SEQUENCE	This SWISS-PROT entrope the Swiss the European Bioinforce use by non-profit modified and this stentiles requires a or send an email to	J. Bac -!- CA -!- PA	MEDLINE-9013033; Pu Hartnett C., Neidle "DNA sequences of ge protocatechuate 3,4- genes and of DNA seq divergence";	Acinetobacter calc Bacteria; Proteoba Acinetobacter. NCBI_TaxID-471; [1] SEQUENCE FROM N.A.	01-FEB-1991 01-FEB-1991 15-JUL-1999 4-CARBOXYMU PCAC.	CIC CAC	30000000000000000000000000000000000000
תו ביין	wiss-in the ropear opear nor ed and ed an	Bacteriol. CATALYTIC 5-OXO-4,5- PATHWAY: 7 SUCCINATE	=BD14: E=901: tt C. equence atecho	obacte ia; P; obacte axID=c	-1991 -1991 -1999 OXYMU	1 A CACICA	
34 T E	is SWISS-PROT entr tween the Swiss I be European Bioinfo by non-profit diffied and this st titles requires a send an email to	C ACT	3 / ADI 30333; Neid: ces of tate 3 E DNA s	er calcroteobar.	(Rel. (Rel. (Rel. (Rel.	ST	67.3 67.3 65.3 65.3 65.3
AAC37152.1; 335119. ocarbons cat: 1 AA; 15324	This SWISS-PROT entry is conbetween the Swiss Institute the European Bioinformatics use by non-profit institute and this statement modified and this statement entities requires a license or send an email to license	acteriol. 172:956-966(1990). CATALYTIC ACTIVITY: 2-CARBOX 5-OXO-4,5-DIHYDROFURAN-2-ACE PATHMAY: THIRD STEP IN THE C SUCCINATE-AND ACETYL-COA IN	MEDLINE-90133 / ADP1; MEDLINE-9013033; PubMed-2298704; Hartnett C., Neidle E.L., Ngai K. "DNA sequences of genes encoding protocatechuate 3,4-dioxygenase: genes and of DNA sequences within	Acinetobacter calcoaceticus Bacteria; Proteobacteria; g Acinetobacter. Acinetobacter. NCBI_TaxID=471; [1] [1] SEQUENCE FROM N.A.	17, Created) 17, Last sequ 38, Last anno	STANDARD;	612 613 666 74 79 173 257 293 425 427
iabol	cop ute itu itu itu see	6(199 2-CAR 2-CAR 1N TH -COA	222 nco	eus cus	eat st st.		
:1; →. catabolism; Lyase 324 MW; 3AEDDE1F	right. of Biod of Biod nstitut ions as s not I greemer sb-sib.	990). ARBOXY-5-OXO- CHE CATABOLIS IN THE BETA	/ ADP1; 0333; PubMed=2298704; 0333; PubMed=2298704; Neidle E.L., Ngai KL., (es of genes encoding Acinet es of genes evider ate 3,4-dioxygenase: evider ate 3,4-dioxygenase; DNA sequences within genes	us. gamma subdivision;	uence otatio KYLASE	ALIGNMENTS PRT; 134	NU5M_ONCMY NU5M_SALSA NU5M_POLOR GLGB_BACCL MTRG_METKA YGGX_HAEIN MBP_CHICK CGIC_ORYSA YIA3_YEAST Y4RF_RHISN YEBS_ECOLI DNAA_BUCAP
Decarboxylas 1C2834A CRC64	and thr and the are no its cont sage by o://www.	ACTALYTIC ACTIVITY: 2-CARBOXY-5-OXO-2,5-DIHYDROFURAN-2-ACTALYTIC ACTIVITY: 2-CARBOXY-5-OXO-2,5-DIHYDROFURAN-2-ACETATE + CO(2). 5-OXO-4,5-DIHYDROFURAN-2-ACETATE + CO(2). 5-OXO-4,5-DIHYDROFURAN-2-ACETATE + CO(2). 5-OXO-4,5-DIHYDROFURAN-2-ACETATE + COTABOLISM OF PROTOCATECHUATE SUCCINATE-AND ACETYL-COA IN THE BETA-KETOADIPATE PATHWAY	STRAIN=BD143 / ADP1; MEDLINE=9013033; PubMed=2298704; Hartnett C., Neidle E.L., Ngai KL., Ornston L.N.; "DNA sequences of genes encoding Acinetobacter calcoaceticus protocatechuate 3,4-dioxygenase: evidence indicating shuffli genes and of DNA sequences within genes during their evoluti	ision; Moraxellacea	update) on update) E (EC 4.1.1.44) (CMD)	ENTS	
•	ough a colla le EMBL outs restrictions restrictions ent is in and for co isb-sib.ch/a	VAN-2-ACCHUATE	aceticus shuffling of evolutionary	ceae;	ð).		P48176 Q9zzm3 Q95918 P30537 O32868 P14048 P15720 P93411 P40558 P55639 P76271
	ugh a collaboration EMBL outstation - estrictions on its n no way and for commercial sb-sib.ch/announce/	TATE =	ng of onary				oncorhynchu salar polypterus bacillus ca methanopyru haemophilus gallus gallus gallus gallus gallus gacharomyc rhizobium sescherichia buchnera ap

Gaps

0,

```
RESULT
Q9Q0E3
ID Q0
AC Q0
DT 0
DT 0
DT 0
OC OC
                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                              Garcia M., Suarez D.L., Crawf
Swayne D.E., Purdue M.L.;
Virus Res. 0:0-0(1997).
EMBL: U85378; AAC40657.1; -
HSSP; P03495; IAIL.
InterPro, IPR000256; -
                                                                                                                                                                                                                                                041651;
041651;
01-JAN-1998
01-JAN-1998
01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9Q0E3;
Q9Q0E3;
01-MAY-2000
                                         Pfam; PF00600; Flu_NS1; 1. ProDom; PD000613; -; 1.
                                                                                                                                        SEQUENCE FROM N.A.
STRAIN-A/TURKEY/WISCONSIN/68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
SEQUENCE
                               Nonstructural protein.
                                                                                                                                                                                  Viruses; ssRNA negative-strand
Influenza virus A and B group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-A/TURKEY/CALIFORNIA/189/66;
MEDLINE-99362763; PubMed-10430948;
Guan Y., Shortridge K.F., Krauss S., Webster R.G.;
"Molecular characterization of H9N2 influenza viruses:
donors of the 'internal' genes of H5N1 viruses in hong
Proc. Natl. Acad. Sci. U.S.A. 96:9363-9367(1999).
                                                                                                                                                                                                               Influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000256; -. Pfam; PF00600; Flu_NS1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             influenza A virus (A/Turkey/California/189/66(H9N2)). Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses; Influ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                    NONSTRUCTURAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P03495; 1AIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=97390;
                                                                                                                                                                                                                                                                                                                                                            197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            constructural protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       196
                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                  1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                           IQRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF156485; AAD52961.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQRFAWG 202
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     229 AA;
                                                                                                                                                                                                                                             (TrEMBLrel. 05, Created)
(TrEMBLrel. 05, Last sequence update)
(TrEMBLrel. 14, Last annotation updat
                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                            203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                 26199 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                     73.5%;
85.7%;
                                                                                                                             Crawford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13,
13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                     Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                               PRT;
                  3B071EC8560AECF3 CRC64;
                                                                                                                                                                                    viruses; Orthomyxoviridae; Influenza A viruses.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAB9B7B86FBC63BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                           J.М.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                               230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          229
                                                                                                                                                                                                                                                                                                                                                                                                                   DB
37;
                                                                                                                           Latimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                update)
                                                                                                                                                                                                                                                                                                                                                                                                                                Length 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
041653
   Ъ
                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Qy
                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                      Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
     Pfam; PF00600; Flu.NS1; 1.
ProDom; PD000613; -; 1.
Nonstructural protein
SEGITERED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
                                                                        EMBL;
                                                                                                                                                      Influenza A virus.
Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
Influenza virus A and B group; Influenza A viruses.
                                                                                                          STRAIN-A/TURKEY/MINNESOTA/3689-1551/81;
Garcia M., Suarez D.L., Crawford J.M.,
                                                                                                                                                                                                                   01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2000 (TrEMBLrel. 14, NONSTRUCTURAL PROTEIN 1.
                                                                                     Virus Res.
                                                                                               Garcia M., Suarez D.L., C
Swayne D.E., Purdue M.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virus Res. 0:0-0(1997).
EMBL; U85381; AAC40663.1;
HSSP; P03495; 1AIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Garcia M., Suarez
Swayne D.E., Purdu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Viruses; ssRNA negative-strand viruses; Orthomyxoviridae; Influenza virus A and B group; Influenza A viruses. NCBI_TaxID-11320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2000 (TrEMBLrel. 14, NONSTRUCTURAL PROTEIN 1.
                                                              HSSP;
                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                     041654;
                                                                                                                                                                                                                                                                                 041654
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nonstructural protein SEQUENCE 230 AA; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR000256; -.
Pfam; PF00600; Flu_NS1; 1.
ProDom; PD000613; -; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-A/DUCK/MICHIGAN/80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       041653;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     041653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Influenza A virus
                                                                                                                                                                                                                                                                                                                                           198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              198 IQRFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                 1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                          IQRFAWG
                                                         U85382; AAC40665.1;
P03495; 1AIL.
                                                                                                                                                                                                                                                                                                                                                                                        Similarity 85. 6; Conservative
                                                                                     0:0-0(1997)
                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                          204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                purez D.L., C
Purdue M.L.;
  25920
                                                                                                                                                                                                                                                                                                                                                                                                                                                     26067 MW;
                                                                                                                                                                                                                                                                                                                                                                                                    73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crawford
  MW;
                                                                                                                                                                                                                                         Created)
Last sequ
                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB Pred. No. 37; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score
Pred.
                                                                                                                                                                                                                                                                               PRT;
4381024D68E06D28 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    38A85BD8E1C5CF96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ð
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230
                                                                                                                                                                                                                                                                                                                                                                                                 DB
37;
                                                                                                           Latimer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Latimer J.W.,
                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                              14;
                                                                                                           J.₩.,
                                                                                                                                                                                                                                                                                                                                                                                                             Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 230;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                           Slemons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Slemons R.D.,
```

0;

Gaps

0,

₽

SO PROPERTY OF THE PROPERTY OF

041651

R.D.,

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                        esult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          num DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OM protein -
                                                                                                                                                                                                                          õ
                                                                                                                                                                                                                                                                                                 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         length: 0
length: 2000000000
                                                                                                                                                                                                                      Match
                 100.0
80.0
80.0
75.6
75.6
75.6
75.6
75.6
75.6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A_Geneseq_0601:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-646-579-1
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62 . Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 18, 2001, 16:50:35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /SIDS8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \(\sids8\)gcgdata/geneseq/geneseqp/aa1980.DAT:
\(\sids8\)gcgdata/geneseq/geneseqp/aa1981.DAT:
\(\sids1\)b8\)gcgdata/geneseqy/geneseqp/aa1982.DAT:
\(\sids1\)b8\)gcgdata/geneseq/geneseqp/aa1983.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIDS8,
                                                                                                                                                                                                                    Length DB
                                                                                                                                                                                                                                                                                                                                                                    /SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                         /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1993.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
                                                                                                                                                                                                                      끕
                                               AAY58874
AAY58876
AAY58877
                                                                                               AAY04868
AAY90994
AAY73418
AAY58875
                                                                                                                                                                     AAY42321
AAY04867
                                                                                                                                                                                                                                                                      SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                jeneseq/geneseqp/AA1988.DAT:*
/geneseq/geneseqp/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Search time 32.41 Seconds (without alignments)
14.964 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         412676
       Acinetobacter-deri
Mycobacterium spec
Mycobacterium spec
Inhibitory clone p
Human secreted pro
Human peptidase NA
                                                                                                                                                                                                                 Description
                                                                                                                                                                                                                                                                                                                                                                                         RESULT
AAY42321
ID AAY4
XX
AC AAY4
AC AAY4
AC AAY4
AC AAY4
XX
DT 06-L
XX
DE AC1n
XX
KW AC1n
KW Creu
        PXX
Claim 12; Page 7; 11pp; English.
                                 Detecting de-myelinating disease or spongiform encephalopathy
                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter; myelin; spongiform encephalopathy; CJD; immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY42321 standard; peptide; 8 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter-derived peptide epitope #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY42321;
```

73.3	73.3	73.3		73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	73.3	75.6	75.6
350	350	350	350	350	350	350	350	350	350	350	350	350	350	350	350	350	350	314	314	314	306	306	287	246	201	106	55	20	19	16	æ	740	705
18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	18	14	3	13	17	13	13	22	22	21	20	14	18	16	21	21	21
	AAW09961	AAW09962	AAW09963	AAW09964	AAW09965	AAW09967	AAW09969	AAW09970	AAW09971	AAW09972	AAW09973	AAW09974	A:AW09975	AAW09976	AAW09977	AAW09978	AAW09968	AAR34544	AAR37873	AAR29623	AAR88559	AAR28646	AAR28644	AAB79732	AAB79733	AAB54338	AAY28579	3214	AAW37707	AAR71029	AAB12947	AAY58870	5887
																											;						٠
HSV-1 (F) protease	V-1 (F) proteas	V-1 (F) p	V-1 (F) proteas) proteas	HSV-1 (F) protease	V-1 (F) proteas	-1 (F) proteas	V-1 (F) proteas	V-1 (F) proteas	t e dene	t e gene prod	e g	es simplex	protease de	UL26 protease dele	nebacterium	ebacterium	pancreatic	creted pept	l enzym	rminal addi	-2 protea	okinin horm	peptidase	Human peptidase NA								

protease

ALIGNMENTS

(first entry)

X X	Creutzfeldt-Ja	Creutzfeldt-Jakob disease; multiple sclerosis; antibody; epitope;	pitope;
×			
SO	Synthetic.		
လ	Acinetobacter sp.	sp.	
XX		•	
PN	WO9947932-A2.		
×			
PD	23-SEP-1999.		
XX			
ΡF	19-MAR-1999;	99WO-GB00876.	
×			
PR	19-MAR-1998;	98GB-0005913.	
×			
PΑ	(UNLO) UNIV I	(UNLO) UNIV LONDON KING'S COLLEGE.	
X			
ΡI	Ebringer A;		
×	,		
DR	WPI; 1999-571874/48.	374/48.	
×			

```
SULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MY04867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
     Claim 32; Fig 19D;
                                          Mycobacterial DNA vectors containing reporter constructs identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                                                                                                            Gicquel B,
                                                                                                                                                                                                                                                                                                                                                              11-SEP-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                        14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             W09909186-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Secreted protein; Mycobacterium; primer; PCR; amplification; probe; hybridisation; detection; vaccine; immunisation; infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY04867
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         diagnosing de-myelinating diseases and spongiform encephalopathies in animals and humans, especially bovine spongiform encephalopathy, multiple sclerosis or Creutzfeldt-Jacob disease in humans. The method is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           obtained from the mammal for immunoglobulin A (IGA) antibodies indicative of infection by Acinetobacter species. This sequence can be used as a test antigen in a kit to detect such antibodies. The method is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the basis for a model for the development of de-myelinating diseases (and an alternative model for the development of spongiform encephalopathies). This model involves the phenomenon of molecular mimicry in which mammals
                                                                                                                                                         N-PSDB; AAX34119.
                                                                                                                                                                                 WPI; 1999-181045/15.
                                                                                                                                                                                                                                                                                                              (INSP ) INST PASTEUR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY04867 standard; Protein; 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              detecting a de-myelinating disease or spongiform encephalopathy in mammals has been developed which comprises testing a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             exposed to certain bacteria containing peptide sequences which mimic myelin peptides, experience an autoimmune response. A novel method for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             encephalopathies such as Creutzfeldt-Jakob disease or in de-myelinating diseases such as multiple sclerosis. Involvement of Acinetobacter forms
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antibodies. Acinetobacter species may
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to natural Acinetobacter peptide epitopes to bind the corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  species of Acinetobacter, which is sufficiently
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence represents a synthetic peptide epitope (#1) derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the early detection of these infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rfsawgae 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                            Lim EM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ä
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            species
                                                                                                                                                                                                                                                                                                                                                              97FR-0011325.
97FR-0010404.
                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-FR01813.
309pp; French
                                                                                                                                                                                                                                                            Pelicic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein sequence 19D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 45;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                            Portnoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be implicated in spongiform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.4e+05;
                                                                                                                                                                                                                                                         Ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 20;
                                                                                                                                                                                                                                                         Goguet de la Salmoniere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resulting in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  conformationally similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       de-myelinating
                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                         ĸ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

Ş

1 RFSAWGAE 8

Matches

Query Match Best Local Similarity

80.0%;

Score 36; Pred. No.

. 90;

20;

Length 527;

Mismatches

ļ,

Indels

. 0;

Gaps

ç

```
2888888
                                                                                                                                               Sd
                                                                                                                                                                               PT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               δõ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               888888x&
                                                                                                                                                                                                                                                                                                                                                                                                                                         XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY04868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                         proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging to the M. tuberculosis complex. The encoded proteins can be used in
                                                                                                                                                                                                                                                                                                                                                                         11-SEP-1997;
14-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted proteins from various Mycobacterium species microorganisms. The encoding nucleotide sequences can be used as primers and probes for methods for detecting and identifying mycobacteria, especially belonging
 Sequence
                                                                                                                                               Claim 32; Fig 19F;
                                                                                                                                                                       Mycobacterial DNA vectors containing reporter constructs -identifying coding or promoter sequences involved in infection-associated protein expression
                                                                                                                                                                                                                                                                                                           Gicquel B,
                                 vaccines
                                                                                                            Sequences AAY04742-Y05000 and AAY07201-Y07204 represent secreted
                                                                                                                                                                                                                                           N-PSDB; AAX34120
                                                                                                                                                                                                                                                              WPI; 1999-181045/15.
                                                                                                                                                                                                                                                                                            Guigueno A;
                                                                                                                                                                                                                                                                                                                                           (INSP ) INST PASTEUR
                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9909186-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mycobacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Secreted protein; Mycobacterium; hybridisation; detection; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mycobacterium species protein sequence 19F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY04868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY04868 standard; Protein; 527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to the M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ||: ||||
rfafwgae 316
                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        tuberculosis complex. The encoded proteins can be used in for immunisation against a bacterial or viral infection.
527 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             500 AA;
                                                                                                                                                                                                                                                                                                             Lim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                               immunisation against a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sp.
                                                                                                                                                                                                                                                                                                                                                                         97FR-0011325.
97FR-0010404.
                                                                                                                                                                                                                                                                                                                                                                                                                        98WO-FR01813.
                                                                                                                                                                                                                                                                                                           EM,
                                                                                                                                          309pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
                                                                                                                                                                                                                                                                                                           Pelicic V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                           Portnoi D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 primer; PCR; amplification; probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20;
                                                                                                                                                                                                                                                                                                    Goguet de la
                              압
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 500
                               viral infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                         Salmoniere
                                                                                                                                                                                                            for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

336 rfafwgae 343

```
screening; lac operon; protease resistant; peptidase resistant; Rop protein; glutathione sulphotransferase; thioredoxin; infection; maltose binding protein; glutathione reductase; antimicrobial;
                                                                                                                   stabilised bioactive peptide; synthesis; screening; lac operon; protease resistant
                                                                                                                              Escherichia coll; E. coll; randomised peptide library; identifica stabilised bioactive peptide; synthesis; intracellular selection;
                                                                                                                                                                                Inhibitory clone p+/-1 peptide sequence SEQ ID NO:100
                                                                                                                                                                                                                           05-SEP-2000
```

AAY90994 standard; Peptide;

(first entry)

identification;

XXXX

밁 Š

9 sawgae 14

3 SAWGAE 8

Query Match
Best Local Similarity
Matches 6; Conserv

Conservative

Mismatches

75.6%; Score 34; 100.0%; Pred. No.

9; Bg

Length 25; Indels

0;

Gaps

0

XXXXXXX

Escherichia coli Synthetic.

W0200022112-A1 20-APR-2000

12-OCT-1999; 99WO-US23731

13-OCT-1998; 14-DEC-1998;

(UYGE-) UNIV GEORGIA RES FOUND INC. (ALTM/) ALTMAN E.

WPI; 2000-317972/27

Identifying recombinantly an antimicrobial bioactive peptide used as therapeutic agent involves transforming a host cell with expression vector with tightly regulable control region and measuring its inhibition

Example 3; Page 77; 135pp; English.

282866

C peptide (BP) involving transforming a cell with an expression vector in ucleic acid sequence encoding a peptide (P), growing the transformed cell under conditions that repress expression of (P) and then inducing its expression which, if is inhibitory to host cell growth, is indicative of BP expression. An antimicrobial peptide from the present inducing its expression which, if its inhibitory to host cell growth, is condition treatable with a peptide drug. The stabilised peptides are also used for inhibiting the growth of a microbial peptides are useful to treat various pathogenic bacterial such as its expression. Streptococci and Enterococci which are the primary causes of nosocomial infections. Movel inhibitor peptides can be used. In turn, to identify additional novel antibacterial peptides can be used. In turn, to identify additional novel antibacterial peptides can be used. In turn, to identify additional novel antibacterial peptides using a construction and can also be used to elucidate potential new drug targets. The inhibitor peptide target which is inactivated is identified to be used to perform the performance inhibited to the prefix are the primary causes in turn, to identify additional novel antibacterial peptides can be used. In turn, to identify additional novel antibacterial peptides using a construction of the performance of the performance inhibited to be performed and the performance of the performance inhibited that are no longer inhibited to be performed and the performance inhibited in the performance and the performance inhibited to be performed and the performance inhibited to be performed and performance inhibited to be performed and performance in performance inhibited to the performance inhibited that are no longer inhibited to be performed and performance inhibited that are no longer inhibited to the performance and the performance inhibited to the performance in the perf by the peptide. These mutants are then mapped in order to precisely determine the protein target that is inhibited. AAA56033 to AAA56100 AAY90964 to AAY90999 are sequences used in the exemplification of the protein target that is inhibited. The present invention describes a method for identifying a bioactive AAA56033 to AAA56106 and

<u>អស់សង់សង់សង់សង់សង់សង់សង់ស</u>

```
Wong
                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; secreted protein; immunostimulatory; haemostatic; cytokine; proliferative; differentiative; chemotactic; chemokinetic; vaccine thrombolytic; antiinflammatory; cytostatic; immunosuppressive;
                                                                                                                                                                                                                                                                                                      14-MAY-1999;
                                                                                                                                                                                                                                                                                                                                      18-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                     W09958642-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY73418 standard; Protein; 343
                                  (GEMY)
                                                                     13-MAY-1999
                                                                                                                                                     11-DEC-1998;
                                                                                                                                                                                      29-SEP-1998;
                                                                                                                                                                                                                                                                     14-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29-FEB-2000
                                                                                                                                                                                                                                        11-SEP-
                                                                                                                                                                                                         SEP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          G
   ,
6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein clone yc48_1 protein sequence SEQ
                                                                                                                                                                      1998;
                                GENETICS INST INC.
 Clark HF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                    98US-0114415.
99US-0248059.
99US-0287150.
                                                                                                                                   98US-0112159
                                                                                                                                                     98US-0111799
                                                                                                                                                                    98US-0103615
                                                                                                                                                                                    98US-0102329
                                                                                                                                                                                                                                    9805-0099843
                                                                                                                                                                                                                                                                                                     99WO-US10843
Fechtel K,
Agostino MJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ID NO:58.
```

Novel polynucleotides and proteins having by make them suitable for treating, preventing conditions in humans or animals having biological activities which reventing or ameliorating medical

WPI; 2000-053095/04.

Claim 67; Page 621-622; 730pp; English

vaccines) or suppressing activity, haematopoiesis regulating activity, tissue growth activity, activin/inhibin activity, chemotactic/ chemokinetic activity, haemostatic and thrombolytic activity, receptor/ ligand activity, anti-inflammatory activity, cadherin/tumour invasion suppressor activity, and tumour inhibition activity. The polynucleotides are also stated to be useful for gene therapy. Therapeutic compositions The present invention describes human secreted proteins encoded by polynucleotides obtained from adult testes, foetal brain, adult brain, brain (foetal and adult), foetal kidney, adult spleen, and adult thymus cDNA libraries. The polynucleotides and proteins are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating medical conditions in humans and animals. Suggested activities include nutritional activity, cytokine and cell proliferation/differentiation activity, immune stimulating (e.g. as

Ä

```
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
            acidic dipeptidase L (NAALAD-ase L) splice variant, predicted from cDNA (see AAZ58309) obtained during 3' RACE amplifications of small intestine, colon, brain and foetal brain cDNA. The splice variant is prematurely terminated compared with the active protein (see AAZ58870) owing to a 173-nucleotide deletion that results in a frame-shift. Several NAALAD-ase L splice variants (see AAY58871-77) have been identified. Their biological significance has yet to be determined, but inactive variants may be used to regulate the
                                                                                                                                                                                                                                                            Claim 11; Fig -; 95pp; English.
                                                                                                                                                                                                                                                                                                                             New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pangalos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (JANC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral neuropathy; Huntington's disease; acute brain injury; multiple sclerosis; peripheral nerve trauma; ischaemia; dementia; gene therapy; diagnosis; nootropic; neuroprotective; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              chromosome 11q12; prostate cancer; neurodegenerative disease; Alzheimer's disease; schizophrenia; ALS; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAALAD-ase L; Naacetylated alpha-linked acidic dipeptidase; chromosome llq12; prostate cancer; neurodegenerative disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human peptidase NAALAD-ase L splice variant (premature termination).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           are also
AAZ52581
                                                                                                                                                                                                                                                                                                                Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAZ58309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiparkinsonian; anticonvulsant; vasotropic; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY58875 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  represent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 rlsawga 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RFSAWGA 7
                                                                                                                                                                                                               present sequence is that of a human N-acetylated alpha-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             φ
                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-182424/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) JANSSEN PHARM NV
of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          presently valuable for veterinary applications. AAZ52475 encode human secreted proteins, and AAY73390 to AAY73500 t human secreted proteins, given in the present invention.
  active
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     343 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neefs JEFM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98GB-0015284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-GB02241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 6..27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "membrane-spanning 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "encoded by TNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peeters DCG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 34; I
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
NAALAD-ase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
```

```
RESULT
AAY58874
CCC XXX PT PXX DR
                                                                                                                                                                                                                                                                                                                PD
                                                                                                                                                                                                                                                                                                                                 XXXX
                                                                                                                                                                                                                                                                                                                                                                           FT FT SXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                XXXXXXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          888888888888888888
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                  New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 11q12; prostate cancer; neurodegenerative disease; Alzheimer's disease; schizophrenia; ALS; Parkinson's disease; peripheral neuropathy; Huntington's disease; acute brain injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L (and splice variant), II and IV polypeptides, cDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as Alzheimer's disease, schizophrenia, ALS, parkinson's disease, peripheral neuropathy, Huntington's disease, acute brain injury,
                                                                                                                                                N-PSDB;
                                                                                                                                                WPI; 2000-182424/16.
N-PSDB; AAZ58308.
                                                                                                                                                                                           Pangalos M,
                                                                                                                                                                                                                       (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                      14-JUL-1998;
                                                                                                                                                                                                                                                                                  14-JUL-1999;
                                                                                                                                                                                                                                                                                                              27-JAN-2000
                                                                                                                                                                                                                                                                                                                                             WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                      Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antiparkinsonian;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       multiple sclerosis; peripheral nerve trauma; ischaemia; dementia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAALAD-ase L; N-acetylated alpha-linked acidic dipeptidase; chromosome 11q12; prostate cancer; neurodegenerative disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY58874;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAY58874 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis, exposure to neurotoxins, peripheral nerve trauma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Note: The present sequence is not shown in the specification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    figure 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ischaemia or dementia (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 faswgae 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptidase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from the NAALAD-ase L sequence given in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                           Neefs JEFM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis; nootropic; neuroprotective;
                                                                                                                                                                                                                                                    98GB-0015284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA,
                                                                                                                                                                                                                                                                                  99WO-GB02241
                                                                                                                                                                                                                                                                                                                                                                                       /note=
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAALAD ase L splice variant (premature termination).
                                                                                                                                                                                                                                                                                                                                                                        /note= "encoded by TNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             anticonvulsant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                    "membrane-spanning domain"
                                                                                                                                                                                         Peeters DCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          544 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 34; DB 21
Pred. No. 2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vasotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               figure 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

The present sequence is that of a human N-acetylated alpha-linked acidic dipeptidase L (NAALAD-ase L) splice variant, predicted from CDNA (see AAZ58308) obtained during 3' RACE amplifications of smale

Claim 11; Fig -; 95pp; English.

```
.dtches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ery Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAALAD-ase L; N-acetylated alpha-linked acidic dipeptidase; human; chromosome 11q12; prostate cancer; neurodegenerative disease; Alzheimer's disease; schizophrenia; ALS; Parkinson's disease; peripheral neuropathy; Huntington's disease; acute brain injury;
WPI; 2000-182424/16.
N-PSDB; AAZ58310.
                                                                                                                                                                                      14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    multiple sclerosis; peripheral nerve trauma; ischaemia; dementia; gene therapy; diagnosis; nootropic; neuroprotective; neuroleptic; antiparkinsonian; anticonvulsant; vasotropic; splice variant.
                                                                                                 (JANC ) JANSSEN PHARM NV
                                                                                                                                             14-JUL-1998;
                                                                                                                                                                                                                                                                         WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human peptidase NAALAD-ase L splice variant (premature termination).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 determined, but inactive variants may be used to regulate the levels of active protein. The invention provides human NAALAD-ase L (and splice variant), II and IV polypeptides, CDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as Alzheimer's disease, schizophrenia, ALS, Parkinson's disease, peripheral neuropathy, Huntington's disease, acute brain injury, multiple sclerosis, exposure to neurotoxins, peripheral nerve trauma, ischaemia or dementia (claimed).
                                                                                                                                                                                                                                                                                                                                                                                 Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY58876 standard; Protein; 578 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             figure 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            have been identified.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             intestine, colon, brain and foetal brain cDNA. The splice is prematurely terminated compared with the active protein AAYS8870) owing to a 91 nucleotide deletion that results in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           410 faswgae 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  frame-shift.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is not shown in the specification but is ed from the NAALAD-ase L sequence given in figure 1 and
                                                            ĭ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Several NAALAD ase L splice variants (see AAY58871-77) Several NAALAD ase L splice variants (see AAY58871-77) ntified. Their biological significance has yet to be
                                                                                                                                           98GB-0015284
                                                                                                                                                                                    99WO-GB02241
                                                                                                                                                                                                                                                                                                                                    /note= "membrane-spanning domain"
100
                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers 6..27
                                                                                                                                                                                                                                                                                                                /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                              "encoded by
                                                          Peeters DCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 34; DB Pred. No. 2.1e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence given in
                                                                                                                                                                                                                                                                                                              TNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
2.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          figure 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
```

New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and

(JANC) JANSSEN PHARM NV

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY58877
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 71.4
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 multiple sclerosis; peripheral nerve trauma; ischaemia; dementia; gene therapy; diagnosis; nootropic; neuroprotective; neuroleptic; antiparkinsonian; anticonvulsant; vasotropic; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAALAD-ase L; N-acetylated alpha-linked acidic dipeptidase; h chromosome 11q12; prostate cancer; neurodegenerative disease; alzheimer's disease; schizophrenia; ALS; Parkinson's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intestine, colon, brain and foetal brain CDNA. The splice variant is prematurely terminated compared with the active protein (see AAY58870) owing to an intronic insertion into CDNA that caused a frame-shift. Several NAALAD-ase L splice variants (see AAY58871-77) have been identified. Their biological significance has yet to be determined, but inactive variants may be used to regulate the levels of active protein. The invention provides human NAALAD-ase L (and splice variant), II and IV polypeptides, CDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as peripheral neuropathy, Huntington's disease, acute brain injury, multiple sclerosis, exposure to neurotoxins, peripheral nerve trauma, is the server of t
                                                                                                                      14-JUL-1999;
                                                                                                                                                                     27-JAN-2000
                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                          WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                     Domain
                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peripheral neuropathy; Huntington's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human peptidase NAALAD-ase L splice variant (premature termination)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY58877;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY58877 standard; Protein; 635 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is that of a human N-acetylated alpha-linked acidic dipeptidase L (NANLAD-ase L) splice variant, predicted from cDNA (see AAZ58310) obtained during 3' RACE amplifications of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         tigure 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The present sequence is not shown in the specification but is derived from the NAALAD-ase L sequence given in figure 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 11; Fig -; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ischaemia or dementia (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 faswgae 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 FSAWGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       578 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                   99WO-GB02241
                                                                                                                                                                                                                                                                                                 /note= "membrane-spanning
                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers 6..27
                                                                                                                                                                                                                                                                      /note= "encoded by TNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 34; DB 21;
Pred. No. 2.2e+02;
2; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acute brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 578;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
acidic dipeptidase L (NANLAD-ase L) splice variant; predicted from cDNA (see AAZ5831) obtained during 3' RACE amplifications of small intestine, colon, brain and foetal brain cDNA. The splice variant is prematurely terminated compared with the active protein (see AAX58870) owing to an intronic insertion into cDNA that caused a frame-shift. Several NANLAD-ase L splice variants (see AAY58871-77) have been identified. Their biological significance has yet to be determined, but inactive variants may be used to regulate the levels of active protein. The invention provides human NANLAD-ase L (and splice variant), II and IV polypeptides, cDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as Alzheimer's disease, schizophrenia, ALS, Parkinson's disease, peripheral neuropathy, Huntington's disease, acute brain injury, multiple sclerosis, exposure to neurotoxins, peripheral nerve trauma, ischaemia or dementia (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                         Alzheimer's disease; schizophrenia; ALS; Parkinson's disease; peripheral neuropathy; Huntington's disease; acute brain injury; multiple sclerosis; peripheral nerve trauma; ischaemia; dementia; gene therapy; diagnosis; nootropic; neuroprotective; neuroleptic; antiparkinsonian; anticonvulsant; vasotropic; splice variant.
WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAALAD-ase L; N-acetylated alpha-linked acidic dipeptidase; human; chromosome 11q12; prostate cancer; neurodegenerative disease;
                                                                                                 Misc-difference
                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human peptidase NAALAD-ase L splice variant (deletion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY58871 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 11; Fig -; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The present sequence is not shown in the specification but is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a human N-acetylated alpha-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ischaemia or dementia (claimed)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 410 faswgae 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 71. les 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                from the NAALAD-ase L sequence given in figure 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
                                                                                          /note= "membrane-spanning domain" 100
                                                                                                                                                                Location/Qualifiers 6..27
                                                           /note= "encoded by TNC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peeters DCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB
Pred. No. 2.5e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.5e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 635;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
RESULT 11
AAY58872
X S X
                                                                                           ₹₹
                                                                                                                                                            222
                                                                                                                                                                                                                                                        XXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ρ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           뮍
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                              NAALAD-ase L; N-acetylated alpha-linked acidic dipeptidase; human; chromosome 11q12; prostate cancer; neurodegenerative disease; Alzheimer's disease; schizophrenia; ALS; Parkinson's disease; peripheral neuropathy; Huntington's disease; acute brain injury; multiple sclerosis; peripheral nerve trauma; ischaemia; dementia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        L (and splice variant), II and IV polypeptides, cDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as Alzheimer's disease, schizophrenia, ALS, Parkinson's disease, peripheral neuropathy, Huntington's disease, acute brain injury, more peripheral neuropathy, exposure to neurotoxins, peripheral nerve trauma, included a scheme of the contraction of t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intestine and colon cDNA. The splice variant carries a deletion of amino acids 161-201 of NAALAD-ase L (see AAY58870). Several NAALAD-ase L splice variants (see AAY58871-77) have been identified. Their biological significance has yet to be determined, but spliced out residues may affect levels of glycosylation and the conformation and activity of the protein. The invention provides human NAALAD-ase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY58872;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY58872 standard; Protein; 705 AA
                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-2000
                                                                                           antiparkinsonian;
                                                                                                                       gene therapy; diagnosis;
                                                                                                                                                                                                                                                                                                                                                       Human peptidase NAALAD-ase L splice variant (deletion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The present sequence is not shown in the specification derived from the NAALAD-ase L sequence given in figure 1 and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ischaemia or dementia (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cDNA (see AAZ58305)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence is that of a human N-acetylated alpha-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pangalos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         369 faswgae 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dipeptidase L (NAALAD-ase L)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fig -; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       699 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Neefs JEFM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99WO-GB02241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         L (NAALAD-ase L) splice variant, predicted from obtained during 5' RACE amplifications of small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   75.68;
71.48;
                                                                                                                       nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peeters DCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 34; DB 21;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                        vasotropic; splice variant
                                                                                                                          neuroprotective; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 699;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
```

Domain

٠ :

Location/Qualifiers

/note= "membrane-spanning domain"

```
Query Match
_ Best Local Similarity
_ ** hes 5; Conserva
              35355555557255
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ₽
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WAMALAD-ase L; N-acetylated alpha-linked acidic dipeptidase; human; chromosome 11q12; prostate cancer; neurodegenerative disease; Alzhelmer's disease; schizophrenia; ALS; Parkinson's disease; peripheral neuropathy; Huntington's disease; acute brain injury; multiple sclerosis; peripheral nerve trauma; ischemia; dementia; gene therapy; diagnosis; nootropic; neuroprotective; neuroleptic; antiparkinsonian; anticonvulsant; vasotropic; splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          amino acids 296-301 of NANLAD-ase L (see ANY58870). Several MANLAD-ase L splice variants (see ANY58871-77) have been identified. Their biological significance has yet to be determined, but spliced out residues may affect levels of glycosylation and the conformation and activity of the protein. The invention provides human NANLAD-ase L (and splice variant), II and IV polypeptides, CDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as peripheral neuropathy, Huntington's disease, acute brain injury, multington account to the content of the conten
                                                                                                                                                                                               Human
                                                                                                                                                                                                                                              08-MAY-2000 ·
                                                                                                                                                                                                                                                                                                                                     AAY58873 standard; Protein; 705 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FSAWGAE 8
|::||||
375 faswgae 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Note: The present sequence is not shown in the specification but derived from the NAALAD-ase L sequence given in figure 1 and
                                                                                                                                                                                                                                                                                              AAY58873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of a human N-acetylated alpha-linacidic dipeptidase L (NANLAD-ase L) splice variant, predicted CDNA (see AAZS8307) obtained during 5' RACE amplifications of intestine and colon cDNA. The splice variant carries a deleting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 11; Fig -; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple sclerosis, exposure to neurotoxins, peripheral nerve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   schaemia or dementia (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 100
                                                                                                                                                                                                                                                                                                                                                                                        12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2000-182424/16
                                                                                                                                                                                           peptidase NAALAD-ase L splice variant (deletion).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98GB-0015284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99WO-GB02241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "encoded by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The splice variant carries a deletion of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peeters DCG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 34; DB 21;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human N-acetylated alpha-linked
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TNC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 705;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels ) 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       trauma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
XX E X E X AC
                                                                                                                                                                                                                                                                                                        В
                                                                                                                                                                                                                                                                                                                                                    γ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PTX
```

```
Query Match
Best Local
                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      out residues may affect levels of glycosylation and the conformation and activity of the protein. The invention provides human NAALAD-ase L (and splice variant), II and IV polypeptides, cDNAs, antisense nucleic acids, vectors, host cells, transgenic organisms, antagonists and agonists. These are useful for treating neural disorders such as Alzheimer's disease, schizophrenia, ALS, Parkinson's disease, peripheral neuropathy, Huntington's disease, acute brain injury, multiple sclerosis, exposure to neurotoxins, peripheral nerve trauma, ischaemia or dementia (claimed).

Note: The present sequence is not shown in the specification but is
     08-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acidic dipeptidase L (NAALAD-ase L) splice variant, predicted from cDNA (see AAZ58307) obtained during 5' RACE amplifications of small intestine and colon cDNA. The splice variant carries a deletion of amino acids 296-301 of NAALAD-ase L (see AAY58870). Several
                                                                                               AAY58870 standard; Protein; 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAALAD-ase L splice variants (see AAYS8871-77) have been identified. Their biological significance has yet to be determined, but spliced out residues may affect levels of glycosylation and the conformation
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 11; Fig -; 95pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  figure 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAZ58307
                                                                                                                                                                                                                            375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pangalos M, Neefs JEFM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27-JAN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                 2 FSAWGAE
|::||||
                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence is that of a human N-acetylated alpha-linked
                                                                                                                                                                                                                       faswgae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-182424/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sapiens
                                                                                                                                                                                                                                                                                                                           Similarity 71.4
5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                    705 AA
                                                                                                                                                                                                                            381
                                                                                                                                                                                                                                                                             æ
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the NAALAD-ase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                99WO-GB02241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note=
100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
6..27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "encoded by TNC
                                                                                                                                                                                                                                                                                                                                                75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "membrane-spanning domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peeters DCG
                                                                                                                                                                                                                                                                                                                           2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is not shown
                                                                                                                                                                                                                                                                                                                                             Score 34; DB 21;
Pred. No. 2.7e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    given
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'n
                                                                                                                                                                                                                                                                                                                                                                  Length 705
                                                                                                                                                                                                                                                                                                                      0;
```

NAALAD-ase L;

N-acetylated alpha-linked acidic

dipeptidase;

Human peptidase NAALAD-ase L.

```
Matches
                                                                                                                                                                                                                                      The present sequence is that predicted for human N-acetylated alpha-linked acidic dipeptidase L (NAALAD-ase L) on the basis of isolated cDNA (see AAZ58304). NAALAD-ase L is predicted to be a type II integral membrane protein with 78% identity and 87% similarity to rat NAALAD-ase L. It is most highly expressed in small intestine, spleen and testis. Several splice variants (see AAX58871-77) were identified during the course of CDNA cloning and RT-PCR gene expression analysis. The invention provides human NAALAD-ase L, II and IV cDNAs and encoded polypeptides, as well as vectors, host cells, transgenic organisms, antisense nucleic acids, agonists and antagonists. These are useful for treating neural disorders such as Albeimer's disease, schizophrenia, ALS, parkingon's disease participated.
                                                                                                                                                                Parkinson's disease, peripheral neuropathy, Huntington's disease, acute brain injury, multiple sclerosis, exposure to neurotoxins, peripheral nerve trauma, ischaemia or dementia (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New human N-acetylated alpha-linked acidic dipeptidases for treating neural disorders e.g. Alzheimer's disease, schizophrenia and Parkinson's disease
                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-182424/16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pangalos M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200004157-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chromosome 11q12; prostate cancer; neurodegenerative disease; Alzheimer's disease; schizophrenia; ALS; Parkinson's disease; peripheral neuropathy; Huntington's disease; acute brain injury; multiple sclerosis; peripheral nerve trauma; ischaemia; dementia; therapy; diagnosis; nootropic; neuroprotective; neuroleptic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (JANC ) JANSSEN PHARM NV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        antiparkinsonian; anticonvulsant; vasotropic
  Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAZ58304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fig 1; 95pp; English.
                                                                                                                            740
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neefs JEFM,
                                                                                                                            B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98GB-0015284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB02241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note-
451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note=
298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "N-glycosylated" 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "N-glycosylated"
492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note "N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note= "encoded by TNC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "membrane-spanning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                    75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "N-glycosylated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "N-glycosylated"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peeters
Score 34; D
Pred. No. 2.
2; Mismatche
     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DCG;
DB 21; 1
2.9e+02;
hes 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          domain"
                                              Length 740;
Indels
```

Gaps

0,

HSV-2 protease substrate

```
AAR71029
ID AAR7
                                                                                                                                          B
                                                                                                                                                                  Ş
BXTXCX
                                                                                                    RESULT 15
                                                                                                                                                                                                                                                               RESULT 14
AAB12947
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PF XX XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γ
                                                                                                                                                                                           Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                   This invention relates to a recombinant baculovirus comprising DNA encoding at least one peptide hormone having helicokinin (HK) activity. The invention includes peptide sequence for three synthetic HK hormones (AAB12945-B12947) these peptides help regulate the physiological processes enabling the growth of Helicoverpa zea (corn earworm) larvae. Infestations of H. zea are a major cause of crop loss. The recombinant baculovirus of the invention containing DNA encoding a hormone with HK activity can be used for controlling populations of H. zea and other related crop pest species. The present sequence represents a synthetic helicokinin III hormone peptide. The peptide is used in the production of the baculovirus of the invention.
                       02-OCT-1995
                                                AAR71029;
                                                                         AAR71029 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New recombinant baculovirus comprising DNA encoding a peptide with helicokinin activity, useful for controlling Helicoverpa other related species -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Crop pest; HK-III.
                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Column 3; 8pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-505106/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Raina AK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (USDA ) US SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US6087165-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Helicokinin hormone (HK-III) peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAB12947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB12947 standard; peptide; 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     23-NOV-2000
                                                                                                                                      1 RFSAWG 6
:|||||
3 kfsawg 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         410 faswgae 416
                                                                                                                                                                                            Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 FSAWGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             related species
                                                                                                                                                                                                                                                              æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Leclerc RF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          helicokinin; hormone; corn earworm; growth retardation;
                                                                                                                                                                                           Conservative
                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0258275
                                                                        Peptide;
                                                                                                                                                                                                        73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vakharia
                                                                        16 AA
                                                                                                                                                                                            ۲
                                                                                                                                                                                                        Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ₿
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ۷Ŋ;
                                                                                                                                                                                                        3.4e+05;
                                                                                                                                                                                                                     DB 21;
                                                                                                                                                                                                                   Length 8;
                                                                                                                                                                                           Indels
                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        zea and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hormone
                                                                                                                                                                                          Gaps
                                                                                                                                                                                        0
```

```
Page 9
```

```
iearch completed: October 18, 2001, 16:51:16
Tob time: 41 sec
                                                                                                                                                                                                        Query Match 73.3%; Score 33; DB 16; Length 16; Best Local Similarity 62.5%; Pred. No. 8.6; Matches 5; Conservative 1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      The sequence is that of a synthetic peptide substrate for the herpes simplex wirus type 2 gene UL26 product, the HSV-2 protease. The peptide may be used to identify compounds which modulate HSV-2 protease activity
                                                                                                                                                                                                                                                                                                                               Sequence 16 AA;
                                                                                                                                                                                                                                                                                                                                                                           See also AAR71017-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New herpes simplex virus (HSV)-2 protease and capsid protein - used to develop prods. for use in the diagnosis and treatment of HSV-2 infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 19; Page 12; 51pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-106803/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Debouck CM, Dilella AG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09506055-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-1993;
23-JUN-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-AUG-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Herpes simplex virus; HSV-2; capsid; UL26 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                1 RFSAWGAE 8
:| ||||
9 kfkmwgae 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93US-0110522.
94US-0264537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US09303.
                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                        0;
```

```
Search time 18.9 Seconds (without alignments)
8.715 Million cell updates/sec
   55, Appli
15, Appli
12, Appli
12, Appli
2, Appli
3, Appli
1, Appli
2, Appli
2, Appli
1, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 8
LENGTH: 8
TYPE: PRT
ORANISM: Helicoverpa zea
US-09-258-275-5
                                                                                                                                                                                                                                                                                          RESULT 2
US-09-167-434-15
Sequence 15, Application US/09167434
Patent No. 6008033
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 5
APPLICANT: Hoog, Susan S.

APPLICANT: Smith, Ward W.

TITLE OF INVENTION: No. 6008033el Proteases, CC
TITLE OF INVENTION: Binding to Said Site, and M.

NUMBER OF SEQUENCES: 18

CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road - P.O. Box 1539

CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 5, Applica
Patent No. 6087165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Raina, Ashok A.
APPLICANT: Leclerc, Robert F.
APPLICANT: Vakharia, Vikram N.
TITLE OF INVENTION: Recombinant Baculovirus
TITLE OF INVENTION: Agent for Crop Pests
FILE REFERENCE: 0140.97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/258,275 CURRENT FILING DATE: 1999-02-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                             1 RFSAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.5
30.5
30.5
30.5
30.5
30.5
30.5
30.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/09258275
                                                 Hoog, Susan S.
Smith, Ward W.
Smith, Ward W.
VENTION: No. 6008033el Proteases, Compositions VENTION: Binding to Said Site, and Methods of USEQUENCES: 18
                                                                                                                                                                    Debouck, Christ
Janson, Cheryl
                                                                                                                                                                                                               Qiu, Xiayang
Culp, Jeffrey
                                                                                                                                                                                                                                                                                                                                                                                                                                                 6
                                                                                                                                                                                                                                                   Abdel-Meguid,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    666666777766666666777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .77
                                                                                                                                                                                           Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%;
                                                                                                                                                                                                                                                   Sherin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55194425-4
US-08-227-372-1
US-08-470-397-1
US-08-470-397-1
US-08-462-351-3
US-09-055-263-1
5194425-3
5468481-3
US-09-137-759-2
US-08-906-769-157
US-08-906-616-157
US-08-906-613-157
US-09-012-431-157
US-09-012-431-157
US-09-012-431-157
US-09-012-431-157
US-09-012-431-157
US-09-012-431-157
US-09-012-431-157
US-09-012-431-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 3; L
Pred. No. 1.5e+05;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Its Use as a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
Patent No.
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                         s Capable of
Use Thereof
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Biocontrol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. Appli
1. Appli
1. Appli
1. Appli
1. Appli
1. Appli
2. Appli
2. Appli
2. Appli
3. Appli
5. 5194425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2, Appli
2, Appli
2, Appli
4, Appli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            157,
157,
157,
157,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
```

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Issued_Patents_AA:*
1: /cgn2_6/ptodata/2,
2: /cgn2_6/ptodata/2,
3: /cgn2_6/ptodata/2,
4: /cgn2_6/ptodata/2,
5: /cgn2_6/ptodata/2,
6: /cgn2_6/ptodata/2,

/cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/backfiles1.pep:*

No

Score

Query Match

Length

Β́

US-09-258-275-5 US-09-167-434-15 US-08-853-755-15 US-08-85-776-12 US-08-251-2808-12 US-09-298-819A-12 US-08-279-754-2

298-819A-12

Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Description

score and is

ce gréater t is derived

No. 1s the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.

10 11 12 13 14 15 16 17 17 18 19 19 20 20 22 22 23 23 24 27

635
1150
11164
11167
1167
1261
7
22
22
22
22
22
22
22
22
22
23
22
23
20
20
20

Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence

5 PCT US95-09052-2
1 US-08-458-067-2
5 PCT US96-07795-2
5 PCT US96-07796-2
1 US-07-832-855-2
2 US-08-589-756-3
2 US-08-589-756-3
2 US-08-589-756-2
3 US-08-589-756-2
3 US-08-589-756-2
4 US-08-589-756-2
5 US-08-252-9668-18
5 US-08-252-9668-18
6 US-08-252-9688-18
7 US-08-258-275-4
7 US-08-310-912A-81
7 US-08-488-5408-11
7 US-08-488-5408-11
7 US-08-488-5408-11

Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence Total number of hits satisfying chosen parameters:

197339 seqs, 20590346 residues

.imum DB

seq

length: length:

: 0 : 2000000000

Perfect score:

US-09-646-579-1 45

RFSAWGAE 8

Title:

protein 000

protein search,

using

SW

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd

October 18,

2001, 16:50:35

٠.

Scoring table:

BLOSUM62 Gapop 10.0 ,

Gapext 0.5

STREET:

709 Swedeland Road -

```
S-09-167-434-15
                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                    est Local s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 610-270-5090
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/024,416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: 610-270-5022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DALE.

PRIOR APPLICATION DATA:

OS 60/030,901
                                                                        APPLICANT:
                                                                                                                  PPLICANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                            PPLICANT:
                                                                                                                             PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 6
                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE: 21-JA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDIUM TYPE: Floppy disk
                                                                                                                                                                                   ŏ.
                                                                                                                                                                                                                                                                  KFKIWGAE 10
                                                                                                                                                                                                                                                                                            RFSAWGAE 8
                                                                                                                                                                    INFORMATION:
                                                                                                                                                                                                                                                                                                                      Similarity 62.5; Conservative
                                                                                                                                                                                   6083711
                                                                                                                                                                                                                                                                                                                                                                                                                                              H: 19 amino acids amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19406-2799
                                            INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pennsylvania
                                                                                               Debouck, Christin
Janson, Cheryl A.
                                                                                                                                         Qiu, Xiay
                                                                      Smith, Ward W.
                                                                                                                                                         Abdel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn Release #1.0, Version #1.30
SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                        peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dara L.
                                                                                   Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                            Jeffrey
                                                                                                                                                      Meguid, Sherin
                                                                                                                                                                                                                                                                                                                                  73.3%;
62.5%;
                                        Binding to
                                                                                                               Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us 60/039,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 60/022,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 60/035,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US/09/167,434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08/853,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          33,680
                                      6083711el Proteases,
ling to Said Site, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P50472-1
                                                                                                                                                                                                                                                                                                                                   Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                        Compositions Capable of
d Methods of Use Thereof
                                                                                                                                                                                                                                                                                                                                                Length 19;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                      0;
```

```
밁
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Thehes 5; Conserv
                                                                                                                                                                            US-07-798-776-12
                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE:
US-08-853-755-15
                                                                                                                                         Sequence 12, App-
                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 60/024,416
FILING DATE: 21-AUG-1996
                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 21-JAN-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
                                                                         TITLE OF INVENTION:
                                                                                                        APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA: US 60/018,616
                                                           UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Dinner, Dara L.
REGISTRATION NUMBER: 33,680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 6 FILING DATE: 27-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                     3 KFKIWGAE 10
                                                                                                                                                                                                                                                                 1 RFSAWGAE 8
                              DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               19406-2799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        King of Prussia
Washington
                                                                                                                                                                                                                                                                                                                                                                                                                             amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pennsylvania
                                                                                                                                                             Application US/07798776
             1001 G Street, N.W., Eleventh Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                          19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       610-270-5090
                                                                                              WELCH, ANTHONY R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PatentIn Release #1.0, Version #1.30
                             Banner, Birch,
                                                                                                                                                                                                                                                                                                                                                                                peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JMBER: US 60/030,901
14-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                               single
                                                                          ASSAYING
                                                                                       HERPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US 60/039,191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US 60/022,470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 us 60/035,973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US/08/853,755
                                                                                       VIRUS PROTEINASE AND METHOD OF
                                                                                                                                                                                                                                                                                                          Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P50472-1
                             McKie & Beckett
                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                        Length 19;
                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                            Gaps
```

0

COUNTRY: U.S.A

```
IS-08-251-288A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: 31-MAY-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                             equence 12,
                                                                                                                                                                                                                                                                                                                                                                                     quence 12, Application US/08251288A
tent No. 6001967
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202) 508-9290
TELEPAX: (202) 508-9299
TELEX: 197430 BBMB UT
INFORMATION FOR SEQ ID NO: 12
                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner & Witcoff
STREET: 1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Rel. CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HERPES PROTEINASE AND METHOD TITLE OF INVENTION: OF ASSAYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                              PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                             UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy
                                                                                                        OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
nes 5; Conserv
                                                                                         SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13 KFKMWGAE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: AMINO ACID STRANDEDNESS: sir TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ENGTH:
CATION NUMBER:
                                                                                                                                                                                 2000
                                                                                                                                                                                                                          Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FOULKE, CYNTHIA
                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      20 amino acids
                                                                                                                                                                                                                                                                                                                                       Gibson, Wade
Welch, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Herpes simplex virus type 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.3%;
                                                           US/08/251,288A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/07/798,776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32,364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 1; Length 20; Pred. No. 8.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1107.07080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
```

TORNEY/AGENT INFORMATION:

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-298-819A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-251-288A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches.
                                                                                                       Sequence 12, Application US/09298819A
Patent No. 6077679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Patent No.
                                                                                INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for CURRENT APPLICATION DATA
TOPOLOGY: 1:
                                                                  SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Gibson, Wade
APPLICANT: Welch, Anthony
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1001 6 50
CITY: Washington
                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KFKMWGAE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
les. 5; Conserv
                                                                                                                                                                                                                                              CLASSIFICATION:
                                                                                                                                                                                                                                                              FILING DATE
                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 202-508-9299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kagan, Sarah A
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                         20001
                                    : 20 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                    g
                                                                                                                                                                                                                                                                                                                                                                                                                            E: Banner & Witcoff
1001 G Street, NW
                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                            IBM Compatible
                         single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       No. 6001967e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF ASSAYING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HERPES PROTEINASE AND METHOD
                                                                                                                                                                                                                                                                                                for Windows Version 2.0
                                                                                                                                    32141
MRR: 01107.46284
                                                                                                                                                                                                                                                                         US/09/298,819A
                                                                                                                                                                                                                   08/251,288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01107.46284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 33; DB
Pred. No. 8.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 20;
```

DB 3;

Length 20;

```
Query Match
Best Local Similarity
"""" 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
Thes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-08-279-754-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3-08-279-754-2
                                                                                                                                                                                                                                                                                                  T-US95-09052-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTINA COUNTINA COUNTINA COUNTINA COMPUTEN FORM:
COMPUTEN TRANSPORT FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy 
                                                                                                                                                                                                                           equence 2, Application GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (908) 594-47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                               TITLE OF INVENTION:
                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                 250 KFKMWGAE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
STRANDEDNESS: dou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: P.O. CITY: RAHWAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: GIESSER, JOANNE M. REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13 KFKMWGAE 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ŏ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2, Application US/08279754
5. 5486470
                                                                                                                                                                                                                                                             Application PC/TUS9509052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   E: JOANNE M. GIESSER
P.O. BOX 2000, 126 E. LINCOLN AVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HALL, DAWN L.
KUO, LAWRENCE C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DARKE,
                                                                                                                                                                                        DARKE, PAUL L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (908) 594-4720
                                                                                                                                                          HALL, DAWN L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (908) 594-3046
JOANNE M. GIESSER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                           LAWRENCE C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               double
                                                                                         PURIFIED HERPES SIMPLEX VIRAL PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PURIFIED HERPES SIMPLEX VIRAL PROTEASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/08/279,754
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
```

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-458-067-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/08458067
                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/458,067
                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
           ATTORNEY/AGENT INFORMATION:
RAME: Glesser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19.
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PC
                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION: NAME: GIESSER, JOANNE M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 KFKMWGAE 257
                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                         COUNTRY: US
ZIP: 07065-0907
                                                                                           CLASSIFICATION:
                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                          STATE:
                                                                                                                                                                                                                                                                                      CITY: Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: P.O. CITY: RAHWAY
                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY: UZIP: 07065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ropology:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIESSER, JOANNE M.
                                                                                                                                                                                                                                                                       New Jersey
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.
                                                                                                                                                                                                                                                                                                   126 East Lincoln Avenue, P.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        306 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                 Register, Robert B.
Shafer, Jules A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĕ
                                                                                                                                                                                                                                                                                                                      Ms. Joanne M. Giesser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
(908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (908)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                вох 2000,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         594-3046
                                                                                                                                                                                                                                                                                                                                                                    AND VECTORS
                                                                                                                                                                                                                                                                                                                                                                                  HERPES SIMPLEX TYPE 1 PROTEASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT/US95/09052
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 E. LINCOLN AVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33;
                                                                                                                                                                                                                                                                                                     Box 2000-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
```

```
CT-US96-07796-2
                :ESULT
                                                                                                                                                                                     CT-US96-07795-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-458-067-2
                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US96-07795-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (908) 594-4720 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                TOPOLOGY: 15
                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                      250 KFKMWGAE 257
                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (908) 594-3046
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                     TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT:
                                                                                                              Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 KFKMWGAE 257
                                                                                                                                                                                                                                                                                                                                          NAME: Giesser, Joanne M. REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                 1 RFSAWGAE 8
                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 07065-0907
                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rahway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application PC/TUS9607795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              i: 350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New Jersey
                                                                                                                                                                                                                                          350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 East Lincoln Avenue, P.O. Box 2000-0907
                                                                                                              Conservative
                                                                                                                                                                                                                                                                                 (908) 594-4720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shafer, Jules A.
VENTION: HERPES SIMPLEX TYPE 1 PROTEASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Register, Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MERCK & CO.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                 protein
                                                                                                                         73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                              PCT/US96/07795
                                                                                                                                                                                                                                                                                                                                         32,838
                                                                                                                                                                                                                                                                                                                             19457
                                                                                                        Score 33; DB 5; Expred. No. 1.4e+02; """ matches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 33; DB 1;
Pred. No. 1.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Version #1.30
                                                                                                                                      Length 350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 350;
                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

Sequence 2, Application PC/TUS9607796

COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COUNTRY: USA

60610

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

ICATION NUMBER: UNG DATE: 19920207

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                          ;; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-07796-2
                                                                                                                                                                                                      US-07-832-855-2
                                                                                                                                                                      Sequence 2, Application US/07832855 Patent No. 5478727
                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
TELEPAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                          CORRESPONDENCE ADDRESS:
                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: ,
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION
                                                                                                                                                                                                                                                                 250 KFKMWGAE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
         STREET: 321 NC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TILE OF INVENTION:
STATE:
                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Giesser, Joanne M. REGISTRATION NUMBER: 32,838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: PCT/US96/07796 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: US
ZIP: 07065-0907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rahway
Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Jersey
                          E: ARNOLD, WHITE & DURKEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      350 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: Ms. Joanne M. Giesser
126 East Lincoln Avenue, P.O. Box 2000-0907
                                                                                                                      Liu, Fenyong
                                                                                                                                        Roizman,
                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Register, Robert
Shafer, Jules A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERCK & CO.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                d) 55.
594-4720
40: 2:
                                                                         Methods and Compositions of a Preparation and Use of A Herpes Protease 15
                                                                                                                                                                                                                                                                                                                                            73.3%;
                                                                                                                                       Bernard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND VECTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HERPES SIMPLEX TYPE 1 PROTEASE MUTANTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Robert B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19457
                                                                                                                                                                                                                                                                                                                                              Score 33;
Pred: No.
                                                                                                                                                                                                                                                                                                                                            4e+02
                                                                                                                                                                                                                                                                                                                                                         Length 350;
                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                            Gaps
```

0;

```
Query Match
Best Local Similarity
5; Consery
                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein $-08-589-756-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     S-08-589-756-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein S-07-832-855-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 3, Application US/08589756
Patent No. 5846547
                                                                                                                                                                                  08-589-756-1
                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                    equence 1, Application US/08589756 atent No. 5846547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08: INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS: LENGTH: 1150 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (312) 245-4961
[NFORMATION FOR SEQ ID NO: :
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 473 RFSSWG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 KFKMWGAE 257
                                                                                                       THE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 635 amino acids TYPE: AMINO ACID TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 RFSAWGAE 8
                                                                                                                                                                                                                                                                  1 RFSAWG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Coolley, Ronald B.
REGISTRATION NUMBER: 27,187
REFERENCE/DOCKET NUMBER: ARCD045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
PE: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (312) 744-0090
                                                                                                                                                                                                                                                                                                                                                                                                                                          single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.3%;
                                                                                                     STREPTOCOCCAL C5a PEPTIDASE VACCINE
                                                                                                                                                                                                                                                                                                                            73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREPTOCOCCAL C5a PEPTIDASE VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/589,756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2:

    Mismatches

                                                                                                                                                                                                                                                                                                                          Score 33; L
Pred. No. 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; I
Pred. No. 2
                                                                                                                                                                                                                                                                                                        лв <u>г,</u>
..5e+02;
.0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5e+02;
                                                                                                                                                                                                                                                                                                                                           Length 1150;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 635;
                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
```

Search completed: October 18, 2001, 16:51:41 Job time: 66 sec

```
밁
                          Qγ
                                                                                                                          ; MOLECULE TYPE: protein US-08-589-756-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-589-756-2
                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-589-756-1
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Applic Patent No. 5846547
                                                      Matches
                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                         APPLICATION NUMBER: UINFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: U
                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1167 amino acids
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
473 RFSSWG 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             473 RFSSWG 478
                                                                                                                                                   TYPE: amino acid
STRANDEDNESS: si
TOPOLOGY: linear
                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                        MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                           1 RFSAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RFSAWG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                      5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                        Application US/08589756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1164 amino acids
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                        Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein
                                                                                                                                                                  single
                                                                  73.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                  STREPTOCOCCAL C5a PEPTIDASE VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 73.3%;
                                                                                                                                                                                                                       US/08/589,756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/589,756
                                                                   Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 33; DB 2;
Pred. No. 4.5e+02;
                                                      Mismatches
                                                                   .5e+02
                                                                               Length 1167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 1164;
                                                     Indels
                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
```

```
Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                  lesult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OM protein - protein search, using sw
                                                                                                                                                                                                                                                                                                                                                                                                                       No.
19
20
21
23
24
25
26
27
28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB DB
                                                                                                                                                                                                                                                                                                                                                                                                                     Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                 Query
Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIR_68:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-646-579-1
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       October 18, 2001, 16:50:35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pir2:*
pir3:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pirl:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pir4:*
                                                                                                                                                                                                                                                                                                                                                                                                                    Length DB
                                                                                                                                                                                                                      637
                                     A72037
D86588
E82372
                                                                                                       B69191
H84700
                                                                             S40559
                                                                                            A85485
                                                                                                                                                                               S09759
                                                                                                                                                                                            20990
                                                                                                                                                    S48497
                                                                                                                                                                 H82141
                                                                                                                                                                                                                                                                                                                                   PN0545
                                                                                                                                                                                                                                                                                                                                                                                                                    IJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mode]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Search time 22.89 Seconds (without alignments) 26.623 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         219241
                 potassium uptake p
hypothetical prote
                                            macromolecule tran
                                                                       l-carnitine dehydrat
carnitine dehydrat
                                                             tolB protein,
                                                                                                                hypothetical prote
conserved hypothet
                                                                                                                                            oxidoreductase hom
                                                                                                                                                           disulfide bond
                                                                                                                                                                                                                            colicin E7 (EC 3.1 capsid protein - h
                                                                                                                                                                                                                                                                                    sugar abc transpor
probable permease
                                                                                                                                                                                                                                                                                                                             aminopeptidase (EC probable aminopept gamma4-crystallin
                                                                                                    hypothetical
                                                                                                                                                                      hypothetical prote
                                                                                                                                                                                                   streptococcal C5a
                                                                                                                                                                                                                 beta-galactosidase
                                                                                                                                                                                                                                                          O-succinylhomoseri
                                                                                                                                                                                                                                                                                                               conserved hypothet
                                                                                                                                                                                                                                                                                                                                                                                                              Description
                                                                                                                                                                                                                                                                       HSV-1 proteinase -
                                                                                                                                                                                                                                                                                                                                                                                    hypothetical
                                                                                                                                                                                                                                                                                                                                                                      hypothetical prote
probable AMINOPEPT
                                                         prob
                                                                                                                                                           for
```

;	4.5	44		5	42	41	40	ı. V) (a	2 0	J (بر در	35	4		اد	3 2	31	30	
Š	۳,	L.	1.0	ن •	<u>ω</u>	31	31	31	ι <u>μ</u>) L) t	بر	31	31	10	ا د	31	32	32	
	9	68.9	00.9	0	68.9	68.9	68.9	68.9	68.9	00.9		9	68.9	68.9	00.9	30	68.9	71.1	71.1	
i i	כאנ	348	967) (267	257	176	175	175	169	1	160	165	165	135	1 6	133	1229.	857	
t	J	N	٨.	,	N	N	N	N	2	K	,	4	N	۳	۲	. 6	ن	N	ນ	
20001	E93617	C83571	T32222	000000	S70643	D82751	S45015	JN0681	JN0682	T01783	CIFGGZ	CAECCO	C45711	ASLJ22	ASLJEW	730040	DNOSAG	A56068	S16133	
nypotnetical prote	d burning or or or or or or	probable binding n	hypothetical prote	dorrenly - phosphace	dollabir - phonice	conserved hypothet	gamma-crystallin M	gamma2-crystallin	qamma3-crystallin	gamma-2-crystallin	gamma-crystallin I	reverse cranscript	TOVOTED TRADECTION	nef protein - equi	nef protein (clone	gammas-crystallin	מס ייינייייייייייייייייייייייייייייייייי	CO-repressor prote	dimethylalycine de	

ALIGNMENTS

```
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Ho Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A;Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G. A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complet A;Reference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                      probable AMINOPEPTIDASE - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
C;Accession: H70629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Watches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: D96684

R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820; 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

R;A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Title: Sequence and analysis of chromosome l of the plant Arabidopsis.
A;Status: preliminary; nucleic acid sequence not shown; translation not shown A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: F12P19.16
A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:AE005173; NID:g6227024; PIDN:AAF06060.1; GSPDB:GN00141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-553 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein F12P19.16 [imported] - Arabidopsis thaliana (c;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 *sequence_revision 02-Mar-2001 *text_change 31-Mar-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A86141; MUID:21016719
A;Accession: D96684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           407 FSAWGAQ 413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82.2%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 37; DB
Pred. No. 44;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
                                                                                                                    Whitehead, S.; Barrell, B.G. tuberculosis from the complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 553;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                  Holroyd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                       geno
```

```
Query Match
Best Local Similarity
"-+-hes 6; Conserv:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: S66427; Aucession: S66427; Ancession: S66427; Ancession: Seemblatt, H.M.; Shoham, G.; Spungin-Bialik, A.; Blumberg, S.; Ancession: J. Blochem. 216, 843-846, 1996; Title: Aminopeptidase from Streptomyces griseus. Primary structure and comprehence number: S66427; MUID:96270734
                                                                                  Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                            Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, Iman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Follon, M.V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Species: Streptomyces griseus:Date: 15-Feb-1997 #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Molecule type: protein
Residues: 1-284 <WAR>
Keywords: alpha-aminoacylpeptide hydrolase; zinc;
                                                                                                                                                         Gene: PA2939
                                                                                                                                                                                                     Cross-references: GB:AE004720; GB:AE004091; NID:g9949032; PIDN:AAG06327.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Accession: S66427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Residues: 1-500 <COL>
:Cross-references: GB:Z84724; GB:AL123456; NID:g3261708; PIDN:CAB06558.1; PID:g1817684
:Experimental source: strain H37Rv
                                                                                                                                                                                        Experimental source: strain PAO1
                                                                                                                                                                                                                                                           Status: preliminary
                                                                                                                                                                                                                                                                                          Reference number: A82950;
                                                                                                                                                                                                                                                                                                           Title: Complete genome
                                                                                                                                                                                                                                                                                                                                 ture 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                 Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genetics:
                                                                                                                                                                                                                            Residues:
                                                                                                                                                                                                                                                                            ccession: B83278
                                                                                                                                                                                                                                                                                                                                                                                                                                                hable aminopeptidase PA2939 [imported] - Pseudomonas aeruginosa (strain PAO1)
                                                                                                                                                                                                                                                                                                                                                                                                                 ce: 15-Sep-2000 #sequence_revision 15-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                   cies: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptidase (EC 3.4.11.-) - Streptomyces griseus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             124
333 RFAWWGAE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       309 RFAFWGAE 316
                                                               Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 6; Conserv
                               1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lpqL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFAWWGAE 131
                                                                                                                                                                                                                         type: DNA: 1-536 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                      в83278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                 Conservative
                                                                                                                                                                                                                                                                                              sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               77.8%;
75.0%;
                                                                                77.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             80.0%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 36;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 35;
Pred. No.
                                                                                  Score 35;
Pred. No.
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         griseus. Primary structure and comparison wit
                                                                                  DB 2;
94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2
                                                                                                                                                                                                                                                                                                                                                              Folger, 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2;
                                                                                                                                                                                                                                                                                                                                                                                                                 #text_change 31-Dec-2000
                                                                                                  Length 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zymogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                              ; Warrener, K.R.; Kas,
                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                              P.;
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                              Hickey,
Larbig,
                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Barra,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                              M.J.; Br
K.; Lim,
```

```
submitted to the EMBL Data Library, July 1999
A;Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome A;Reference number: A75001
                                                                                      sugar abc transporter binding protein related PAB2439 - Pyrococcus abyssi (strain C;Species: Pyrococcus abyssi C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                               Ş,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: gamma4 cry
A;Introns: 37/3; 85/3; 126/3
C;Superfamily: beta-crystallin
C;Keywords: duplication
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gamma4-crystallin - African clawed frog (fragment)
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
PN0545
                                                                          C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:AE002066; GB:AE000513; NID:g6460163; PIDN:AAF11904.1; PID:g646
A;Experimental source: strain R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-357 <WHI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S.; Smith, H.O.; Venter, J.C
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; White, O.; Eisen, J.A.; Heidelberg, J.F.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: E75284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DЪ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-172 <SMO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: PN0545
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Characterization of Xenopus laevis gamma-crystallin-encoding genes A;Reference number: JN0680; MUID:93292986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene 128,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R; Smolich,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                              A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: E75284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Genome sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local s
Matches 6
                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                  Gene: DR2359
                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                             123 RFNAWGGK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151 RFSDWGA 157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 RFSAWGA 7
                                                                                                                                                                                                                                                               1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the authors translated the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    189-195, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B.D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PN0545
                                                      Genoscope
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tarkington, S.K.; Saha, M.S.; Stathakis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A75250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.C.; Fraser,
                                                                                                                                                                                                                                                                                                                      75.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               75.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the radioresistant bacterium Deinococcus {\tt MUID:20036896}
                                                                                                                                                                                                                                                                                                    ņ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                      Score 34;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon CAT for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    n, P.; Hickey, E.K.; in, P.; McDonald, L.; II+
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31-Dec-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
48;
                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      residue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 #text_change 17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change 21-Nov-1997
                                                                                                                                                                                                                                                                                                                                       Length 357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 172
                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Peterson,
Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gln
                                                                                                                                                                                                                                                                                                    0,:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J.D.; Dodson, R.J
T.; Zalewski, C.;
                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      for
                                                                                                                                                                                                                                                                                                    0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    residu
```

KFKMWGAE

257

```
Query Match
Best Local Similarity
"hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                 toy-1 proteinase - human herpesvirus 1
                                                                                                                                                                                                                      t;Darke, P.L.; Chen, E.; Hall, D.L.; Sardana, M.K.; Vel
. Biol. Chem. 269, 18708-18711, 1994
. Title: Purification of active herpes simplex virus-1
. Reference number: A54862; MUID:94308117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adman, S.; Yuan, Y.; Brody,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable permease of ABC taurine transporter PA3936 (imported) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: PAB2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AJ248283; GB:AL096836; NID:g5457433; PIDN:CAB49115.1; PID:g54576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-545 < KAW>
                                                                                                                             Superfamily: varicella-zoster virus gene 33 protein
                                                                                                                                                                                            Reference number: A54862;
Accession: A54862
Status: preliminary
                                                                                                                                                                                                                                                                                               Species: human herpesvirus 1;Date: 07-Jul-1995 #text_change 16-Feb-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Reference number: A82950; Accession: D83154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Residues :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Status: preliminary
                                                                                                                                                 Cross-references: GB:L32018
                                                                                                                                                               Molecule type: DNA Residues: 1-306 <DAR>
                                                                                                                                                                                                                                                                                            Accession: A54862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;Superfamily: Synechococcus nitrate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: PA3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cross-references: GB:AE004811; GB:AE004091; Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: Pseudomonas aeruginosa
ate: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .cover, C.K.; Pham, X.Q.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cession:
                                                                                                                                                                                                                                                                                                                                                                                                                   267 RFAAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
les 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity hes 5; Conserver
                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RFSAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RFSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KFSAWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1-272 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D83154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                source: strain Orsay
                                                                                                                                                                                                                                                                                                                                                                                                                                                  6
                                                                                                                                                                                                                                                                                                                                                                                                                   272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            73.3%;
                                                                     73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Erwin, A.L.; Mizoguchi, S.D.;
L.L.; Coulter, S.N.; Folger,
                                                                   Score 33; DB 2;
Pred. No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 34;
Pred. No.
                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        transport
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB
                                                                                                                                                                                                                                                                  M.K.; Veloski, C.A.; LaFemina,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NID: 99950116; PIDN: AAG07323.1; GSPDB: GN00:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .4e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein nrtB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2
                                                     2;
                                                                                Length 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 545
                                                                                                                                                                                                                                      protease expressed in
                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             K.R.; Kas,
                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            an opportunistic patho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P.;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hickey,
Larbig,
                                                  0,
                                                                                                                                                                                                                                      Escherichi
                                                                                                                                                                                                                                                                   R.L.; Shaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         M.J.; Br
K.; Lim,
Query Match
Best Local Similarity
"-+ ohes 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
```

```
A; Genome: plasmid ColE7-K317
C; Superfamily: cloacin DF13 protein
C; Keywords: bacteriocin; endonuclea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
S22453
                                                           A;Gene: cea
                                                                                    A;Cross-references: EMBL:X63620; NID:g510384; PIDN:CAA45164.1;
                                                                                                                                                                                                    submitted to the EMBL Data Library, December 1991
                                                                                                                                                                                                                                                                                                                                   Mol. Gen. Genet. 233, 177-183, 1992
A;Title: Characterization of the cea gene
A;Reference number: S22453; MUID:92293113
                                                                                                                 A;Molecule type: DNA
A;Residues: 371-576 <LAU>
                                                                                                                                                      A; Accession:
                                                                                                                                                                     A; Description: Nucleotide sequence A; Reference number: S49176
                                                                                                                                                                                                                       R; Lau, P.C.K.; Parsons, M.
                                                                                                                                                                                                                                         A;Cross-references: EMBL:M62409; NID:g144374; A;Note: the authors translated the codon GAA /
                                                                                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-576 <SOO>
                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                               C;Date: 04-Dec-1992 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        colicin E7 (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Keywords:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Title: Analysis of corynebacterium glutamicum methionine biosynthetic pathway: A; Reference number: 224410; MUID:99347339
A; Accession: T47234
                                                                                                                                                                                                                                                                                                                       A; Accession: S22453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Pathway: methionine biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AF126953; NID:g5852461; PIDN:AAD54070.1; PID:g5852462
A;Experimental source: strain ASO19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Date: 20-A
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Hwang,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Species: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               O-succinylhomoserine (thiol)-lyase (EC 4.2.99.9)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N; Alternate names:
                                                                                                                                                                                                                                                                                                                                                                                           Soong, B.W.; Lu, F.M.; Chak, K.F.
                                                                              Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Note: cofactor pyridoxal-phosphate
Superfamily: O-succinylhomoserine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ang, B.J.; Kim, Y.; Kim, H.B.; Hwang, H.J.; Kim, Cells 9, 300-308, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  118 FTAWGVE 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
les 5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 FSAWGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    metB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-Apr-
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  carbon-oxygen
                                                                                                                                                    S49179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-386 <HWA>
                                                                                                                                                                                                                                                                                                                                                                                                                  S22453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T47234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3.1.21.-) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EC 4.2.99.9 [validated;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 000 #sequence_revision 20-Apr-2000 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cystathionine
                                                                                                                                                                                                                                                                                                                                                                                                                S49179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              translated
endonuclease; hydrolase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 33; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gamma-synthase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from
                                                                                                                                                                                   encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (thiol)-lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M1smatches
                                                                                                                                                                                                                                                                                                                                                                                                                              24-Apr-1998 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  coli plasmid ColE7-K317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUID:99347339]
                                                                                                                                                                                                                                                                                                                                                        of the
                                                                                                                                                                               the immunity and lysis proteins
                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DВ
                                                                                                                                                                                                                                       PIDN:AAA98054.1; PID:g144375 for residue 366 as Phe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5e+02;
                                                                                                                                                                                                                                                                                                                                                        ColE7
toxin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [validated] - Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.H.;
                                                                                                                                                                                                                                                                                                                                                    plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              11-Jun-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                 and the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glutam
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              isol
```

Conservative

73.3%; 83.3%;

Score 33; DB 1; Le Pred. No. 2.2e+02; 1; Mismatches 0;

Length 576;

Indels

0;

Gaps

0;

```
Query Match
Best Local Similarity
"-+-hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      eta-galactosidase (EC 3.2.1.23) isozyme 12 -
       Chen, C.C.; Cleary, P.r. 265, 3161-3167, 1990
                                                                                                          reptococcal C5a peptidase (EC 3.4.21.-) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McGeoch, D.J.; Dalrymple, M.A.; Davison, A.J.; Dolan, A.; Frame, M.C.; McNab, D.; F. Gen. Virol. 69, 1531–1574, 1988; Title: The complete DNA sequence of the long unique region in the genome of herpes. Reference number: A30083; MUID:88274327; Accession: H30084
                                                        Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 Accession: A35066; S52539
                                                                                                                                                                                                                                                                                                                                                              Cross-references: GB:U17417; NID:g676845; Superfamily: Bacillus beta-galactosidase Keywords: glycosidase; hydrolase
                                                                                                                                                                                                                                                                                                                                                                                                                     Molecule type: DNA
Residues: 1-637 <GUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Superfamily: varicella-zoster virus gene 33 protein Keywords: capsid protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Species: human herpesvirus i
Date: 31-Dec-1989 #sequence_revision 31-Dec-1989 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 03-Oct-1995 #sequence_revision 03-Oct-1995 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Arthrobacter sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  residues: 1-635 <MCG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene: UL26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cross references: GB:X14112; NID:g1944536; PIDN:CAA32318.1; PID:g59526; GB:D00317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tus: nucleic acid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RFSAWG 6
:|||||
123 KFSAWG 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250 KFKMWGAE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 RFSAWGAE 8
                                                                                                                                                                                                      245 RFSSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                  14
                                                                                                                                                                                                                                        1 RFSAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          12
   Chem. 265,
Complete n
                                                                                        Streptococcus pyogenes
                                                                                                                                                                                                      250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human herpesvirus 1 (strain 17)
herpesvirus 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                            Conservative
nucleotide sequence of the streptococcal C5a peptidase gene of Streptd
                                                                                                                                                                                                                                                                                           73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     not shown; translation not shown
                                                                                                                                                                                                                                                                        Score 33; DB 2;
Pred. No. 2.5e+02;
1; Mismatches C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 33; DB 1; Length 635
Pred. No. 2.5e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                PIDN:AAA75601.1; PID:g676846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arthrobacter sp.
                                                                     #text_change 18-Jun-1999
                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                        Length 637
                                                                                                         Streptococcus pyogenes
                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  17-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from a psychrotrophic
                                                                                                                                                                                                                                                                        ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B7)
                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.; Per
밁
                               Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ş
```

```
A;Cross-references: EMBL:X17403; NID:g59591; PIDN:CAA35300.1; PID:g1780920
A;Note: this sequence was submitted to the EMBL Data Library, December 1989
C;Keywords: glycoprotein; transmembrane protein
F;1-25/Domain: signal sequence *status predicted <SIG>
F;26-171/Product: hypothetical protein IRLIO *status predicted <MAT>
F;70-103/Domain: transmembrane *status predicted <TMM>
F;48,49,56,108/Binding site: carbohydrate (Asn) (covalent) *status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Note: host Homo sapiens (man)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 08-Oct-1999
C;Accession: S09903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypothetical protein IRL10 precursor - human cytomegalovirus C; Species: human cytomegalovirus, human herpesvirus 5
                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-171 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Curr. Top. Microbiol. Immunol. 154, 125-169, 1990 A; Title: Analysis of the protein-coding content of the sequence A; Reference number: S09749; MUID:90269039
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;130,193,512/Active site: Asp, His, Ser #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Molecule type: DNA
A;Residues: 1-75,'V',77-78,'K',80-83,'PS' <KAT>
A;Cross-references: GB:S75411; NID:g914107; PIDN:AAB33264.1; PIL:g914112
A;Note: in Genbank entry S75411, release 106.0, the initiation codon TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Katerov, V.; Schalen, C.; Totolian, A.A.
Mol. Gen. Genet. 245, 78-85, 1994
A;Title: Sequencing of genes within the vir regulon of Streptococcus pyogenes type
A;Reference number: S52535; MUID:95147851
A;Accession: S52539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       F;1034-1101/Region: glycine/proline-rich 17-residue repeats F;1040-1157/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: GB:J05229; NID:g153776; A;Note: the amino end of the mature protein R;Katerov, V.; Schalen, C.; Totolian, A.A.
                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: S09903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;1-31/Domain: signal sequence #status predicted <SIG>F;32-1167/Product: streptococcal C5a peptidase #status predicted <MAT>F;32-156/Domain: subtilisin homology #status atypical <SBT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Description: specifically cleaves a Lys-Asp peptide bond near the carboxyl end C;Superfamily: streptococcal C5a peptidase; subtilisin homology C;Keywords: cell wall; hydrolase; serine proteinase; tandem repeat; transmembranc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: DNA
A;Residues: 1-1167 <CHE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A35066; MUID:90153964
A;Accession: A35066
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;1029-1139/Domain: cell wall spanning #status predicted <CWS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: scpA
A;Start codon: TTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Chee, M.S.; Bankier, A.T.; Beck, S.; Bohni, R.;
   Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Species: human cytomegalovirus, human herpesvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Function
                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               473 RFSSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 RFSAWG
      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1;
                               Score 32; DB 2;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 33; DB 1;
Pred. No. 4.4e+02;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             was determined by protein sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PIDN: AAA26960.1; PID: 9552009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brown,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1167;
                                                        Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tandem repeat; transmembrane pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C.M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (strain AD169)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cerny,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of
   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.; Horsnell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for residue
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of h
```

78 YSAWGA

83

2 FSAWGA 7

Search completed: October 18, 2001, 16:52:11 Job time: 96 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OM protein - protein search, using sw model
      Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and 1s derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                              Query
Match
   SwissProt_39:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93435 seqs, 34255486 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BLOSUM62 . Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 18, 2001, 16:50:35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-09-646-579-1
45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                              В
CRGA_XENLA
CEA7_ECOLI
VP40_HSVII
SCPA_STRPY
1R10_HCMVA
DSBB_VIBCH
XIV5_YEAST
CAIB_ECOLI
TOLB_CHLPM
DHM1_PARDE
CSP1_CORGL
M2GD_RAT
CRG5_XENLA
REV_EIAV9
REV_EIAV6
REV_EIAV6
REV_EIAV6
REV_EIAV7
CRG2_RANTE
CRG2_XENLA
APXA_PORGI
MP01_DROME
ECHB_MYCLE
PEXC_ARATH
Y4CF_RHISN
V382_ASFL5
GUN1_BCHL7
GUN3_CHT7
GUN3_CHT7
FUR8_ARCFU
PUR8_ARCFU
PUR8_BACSSU
                                                                                                                                                                                                                                                                                                                                                                                                     APX_STRGR
                                                                                                                                                                                                                                                                                                                                                                                                                              ij
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Search time 12.81 Seconds (without alignments)
21.393 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93435
                                                                                                                                              P11305 equine infe
P32543 equine infe
P20919 equine infe
P20919 equine infe
P02531 rana tempor
P48649 chiloscylli
Q91724 xenopus lae
P55940 xenopus lae
                        084604
028041
Q58339
                                                           Q9m841
P55388
P26712
P54424
                                                                                                            Q51843
Q9vmw8
Q07137
                                                                                                                                                                                                                                                                                                                     P15926 streptococc
P16808 human cytom
O9kqu6 vibrio chol
                                                                                                                                                                                                                                   Q06255 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                  P80561 streptomyce
P55941 xenopus lae
                                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                                                                                                                                                                        Q47112 escherichia
                                                                                                                                                                                                                                                                                               79 saccharomyc
72 escherichia
                                                                                                                                                                                                                                                2 rattus norv
                   3 porphyromon
8 drosophila
7 mycobacteri
1 arabidopsis
8 rhizobium s
2 african swi
4 ustilago at
4 ustilago t
1 archaeoglob
9 methanococc
                                                                                                                                                                                                                                                           d chlamydia p
3 paracoccus
7 corynebacte
                                                                                                                                                                                                                                                                                                                                                            herpes simp
```

	35 35 35 37 44 42 42 43 44 43
	30.55 30.55
	68.9 68.9 68.9 68.9 68.9 67.8 67.8
	682 725 939 938 1013 1046 1216 1840 1847 169 171
ALIGNMENTS	ATKB_ECOLI TAP1_RAT EAE1_ECOLI PPOL_XENLA PPOL_SIVAG ALA4_ARATH AFP1_ARATH MBP_BOVIN MBP_BOVIN MBP_PANTR
	P03960 escherichia P36370 rattus norv P19809 escherichia P31669 xenopus lae P37008 rattus norv P27980 simian immu Q91nq4 arabidopsis P18616 arabidopsis P18616 arabidopsis P18616 pan troglod P81558 sus scrofa

FT	00 00 g g	ននន	3888	R R R	RA RA	RR RT	RA RA	RA RT RL RN	R R R R R R R R R R R R R R R R R R R	RA RA	2222	RE ID AC
	-!- SUBCELLULAR LOCATION: SECRETED!- MASS SPECTROMETRY: MW-29728; MW_ERR-1.0; -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY N PDB; 1XJO; 01-App-97. MEROPS: M28,003.	-!- ENZYME REGULATION: BINDS ACTIVITY OF THE ENZYME!- SUBUNIT: MONOMER.		acti Eur.	CHARACTERIZATION. MEDLINE-93185612; PubMed-8444149; Ben-Meir D., Spungin A., Ashkenazi R., Blumberg	"streptomyces griseus aminopeptidase: X-ray structure at 1.75-A resolution."; J. Mol. Biol. 265:620-636(1997).		Spungin A., Blumberg S.; Spungin A., Blumberg S.; "Streptomyces griseus aminopeptidase is a metalloprotein. Purification and propertie Eur. J. Biochem. 183:471-477(1989). [3]	comparison with other zinc-containing amin Eur. J. Biochem. 236:843-846(1996). [2] SEQUENCE OF 1-6.			RESULT 1 APX_STRGR ID APX_STRGR STANDARD; PRT; 284 AA. AC PR0561.
m; 3D-structure.	METHOD-ELECTROSPRAY. 128B.	MODULATES THE	IDS, ESPECIALLY DUE IS PROLINE.	lase and modulation of itution.";	ιο · · · · · · · · · · · · · · · · · · ·	crys tallographic	alik A., Barra D.,	calcium-activated zinc s of the enzyme.";	primary structure and opeptidases.";	ialik A., Blumberg S.,	teridae; ceae; Streptomyces.	

В

151

RFSDWGA 157

```
Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              _XENLA
                                                                                                                                                                                                                             Eye lens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
METAL
METAL
DISULFID
SEQUENCE
                                                                                                                                                                                                                                    EMBL; M99582; -; NOT_ANNOTATED_CDS.
HSSP; P02526; IGCS.
InterPro; IPR001064; -.
Pfam; PF00030; crystall; 2.
PROSITE; PS00225; CRYSTALLIN_BETAGAMMA; 4.
Eye less protein; Duplication; Multigene f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gene 128:189-195(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE=93292986; PubMed=8514186;
Smollch B.D., Tarkington S.K., Saha M.S., Stathakis D.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Amphibia; Batrachia; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae; Xenopodinae; Xenopodinae; Xenopos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel...35, Created)
01-NOV-1997 (Rel...35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
01-NOV-1997 (Rel. 35, Last annotation update)
GAMMA CRYSTALLIN IV (GAMMA-4-CRY) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                     modified and this statement is not removed. entitles requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                      the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Grainger R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 *Characterization of Xenopus laevis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            124 RFAWWGAE 131
                                                Local Similarity
hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 RFSAWGAE
1 RFSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VERY SIMILAR GREEK KEY MOTIFS.
SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: MONOMER (BY SIMILARITY).

DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OF THE VERTEBRATE EYE LENS.
SUBUNIT: MONOMER (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _XENLA
                                                                                                                                                                                                                                                                                                                                                                                                       non-profit
                                                                                                                             <1
38
82
86
127
172 AA;
                                              75.6%;
nilarity 85.7%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         132
160
247
245
284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              132
160
247
250
29722 .
                                                                                                                                              1
37
81
85
126
172
                                                                                                                               21274
                                                                                                                                                                                                                                                                                                                                                                                                     institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          77.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                               ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ARE THE DOMINANT STRUCTURAL COMPONENTS
                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                            MOTIF 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZINC
ZINC
ZINC
                                              Score 34; DB 1; Length 172;
Pred. No. 16;
D; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35; DB
Pred. No. 17;
                                                                                                                                                                           MOTIF 2.
CONNECTING PEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           67F1B80F8CA5C4CC CRC64;
                                                                                                                             1A0BBDE094F9A6AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gamma-crystallin-encoding genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             172
                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                  There are no
                                                                                                                                                                                                                                         family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                      Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOLDED INTO FOUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 284;
                                                                                                                                                                                                                                                                                                                                                                                                                  he EMBL outstation restrictions on it
                                              0,
                                                                                                                                                                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                       commercia.
                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
```

Query Match
Best Local Similarity
"~+~hes 5; Conservations

Conservative

73.3%;

Score 33; DB Pred. No. 75;

1;

Length 576;

Mismatches

0;

Indels

0;

Gaps

0

```
EMBL; M62409; AAA98054.1; -
EMBL; X63620; CAA45164.1; -
PDB; 7CEI; 17-SEP-99.
InterPro; IPR002711; -
InterPro; IPR003058; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CEA7_ECOLI STA
Q47112; Q51604;
30-MAY-2000 (Rel.
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KO T.P., Liao C.C., Ku W.-Y., Chak K.-F., Y "The crystal structure of the DNase domain with its inhibitor Im7 protein."; Structure 7.91-102(1999).
                                                           Zinc;
METAL
                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -i- FUNCTION: COLICINS ARE POLYPEPTIDE TOXINS PRODUCED BY AND ACTIVE AGAINST, ESCHERICHIA COLI AND CLOSELY RELATED BACTERIA.
-i- SIMILARITY: BELONGS TO THE NUCLEASE FAMILY OF COLICINS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli. Plasmid ColE7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLE7 OR CEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2000 (Rel. 4
COLICIN E7 (EC 3.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ECOLI
                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                          entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: THIS PLASMID-CODED BACTERICIDAL PROTEIN IS AN ENDONUCLEASE ACTIVE ON BOTH SINGLE-AND DOUBLE-STRANDED WITH UNDEFINED SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-99148115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=K317;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Gen. Genet.
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria;
Escherichia.
                                                                                                    Antibiotic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Nucleotide sequence encoding the immunity and lysis proteins and the carboxyl-terminal peptides of colicins E4 and E7."; Submitted (DEC-1991) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lau P.C.K., Parsons M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 371-576
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=562;
                                                                                                                                            Pfam; PF01844; HNH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                     PYOSINS.
                                                         iotic; Bacteriocin; Plasmid; Hydrolase; Endonuclease;
Metal-binding; 3D-structure.
544 544 ZINC.
                                                                                                                     PR01295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
  ΑΑ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                       CLOACIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          39, Last
40, Last
1.21.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed-10368275
                     573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
  61349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gamma subdivision; Enterobacteriaceae;
                   ZINC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
E5B05E73B2E17249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 576
                                                                                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               update)
                                                                                                                                                                                                                                                                                                                                               There are no restrictions on 
ng as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ŗ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cole7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yuan H.S.;
n of colicin
                                                                                                                                                                                                                                                                                                                       Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasmid.";
CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  in complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA
                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BUT
```

문 S

123

KFSAWG

128 ģ

RFSAWG

۳.

Length 635;

```
PROCESS OF THE PROCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
VP40_H
                                     SITE
ACT_SITE
ACT_SITE
ACT_SITE
                                                                                                                                               PROPEP
SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                  SEQUENCE
                                                                                                                                                                                                                                                                                                   PRINTS; PR00236; HSVCAPSIDP40:
Coat protein; Hydrolase; Serine
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; D10879; BAA01672.1;
EMBL; X14112; CAA32318.1;
PIR; H30084; WMBEW6.
HSSP; P16753; ICMV.
                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
01-GT-1996 (Rel. 34, Last annotation update)
01-OCT-1996 (Rel. 34 (VIRION STRUCTURAL PROTEIN
CAPSID PROTEIN P40 (VIRION STRUCTURAL PROTEIN
CAPSID PROTEIN P40 (PROTEASE) (EC 3.4.21.-); CAPSID
                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       McNab D., Perry L.J., Scott J.E., Taylor P.;
"The complete DNA sequence of the long unique region i herpes simplex virus type 1.";
J. Gen. Virol column
                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR001847; -
                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; S21.001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Davison M.D., Rixon F.J., Davison A.J.;

'Identification of genes encoding two capsid proteins (VP24 and of herpes simplex virus type 1.";

J. Gen. Virol. 73:2709-2713(1992).

-I- FUNCTION: VP22A IS A COMPONENT OF THE CAPSID CORE INVOLVED PROCESSING AND PACKAGING OF PROGENY DNA. VP24 IS A PROTEASE WHICH CAN PROTEOLYTICALLY CLEAVE ITSELF AND VP22A AT THE C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 11-29; 77-91 AND 223-241.
MEDLINE-93019027; PubMed-1328483;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herpes simplex virus (type 1 / strain 17).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _HSV11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-88274327; PubMed-2839594;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alphaherpesvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P10210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VP40_HSV11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PTM: VP22A IS PHOSPHORYLATED.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S21 (SERINE PROTEASE).
SIMILARITY: TO OTHER HERPESVIRUSES CAPSID PROTEIN VP40.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATALYTIC ACTIVITY: PREFERENTIALLY CLEAVES
                                                                                                                                                                                                                                                                                                                                                    PF007-16; Peptidase_S21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Virol. 69:1531-1574(1988).
                                                                                                                    248
7611
247
610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                 635
247
7610
635
248
611
                66470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Simplexvirus
                ¥
CAPSID PROTEIN VP24 (PROTEASE).
CAPSID PROTEIN VP22A.
C.TERMINAL PEPTIDE.
CLEAVAGE (BY THE PROTEASE) (PROBABLE).
CLEAVAGE (BY THE PROTEASE) (PROBABLE).
CLEAVAGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
                                                                                                                                                                                                                                             GENE UL26 PROTEIN.
GENE UL26.5 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                           protease; Phosphorylation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           capsid proteins (VP24 and VP26)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                There are no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UL26) [CONTAINS: CAPSID PROTEIN VP22A].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              24 IS A PROTEASE
VP22A AT THE C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ALA- | -SER OR ALA- | -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  γd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             in the genome of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Frame M.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OH:
```

```
THE FIRST STATES OF THE PROPERTY OF THE PROPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
SCPA_STRPY
ID SCPA_S
AC P15926
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                        PRINTS; PR007/23; SUBTILASE_ASP; 1.
PROSITE; PS00136; SUBTILASE_HIS; 1.
PROSITE; PS00138; SUBTILASE_SER; 1.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
PROSITE; PS00343; GRAM_POS_ANCHORING; FALSE_NEG.
                                                                                                                  ACT_SITE DOMAIN
                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                             TRANSMEM
DOMAIN
                       REPEAT
REPEAT
                                                                     DOMAIN
REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00746; Gram_pos_anchor; Pfam; PF00082; Peptidase_S8; 4. PRINTS; PR00723; SUBTILISIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          *Complete nucleotide sequence of the streptococcal C5a peptidase gene of Streptococcus pyogenes.";
J. Biol. Chem. 265:3161-3167(1990).
-I- FUNCTION: THIS VIRULENCE FACTOR OF S.PYOGENES SPECIFICALLY CLEAVES THE HUMAN SEROM CHEMOTAXIN C5A AT LYS(68)-ASP(69) BOND NEAR ITS C-TERMINUS, DESTROYING ITS ABILITY TO SERVE AS A CHEMOATTRACTANT.
-I- SUBCELLULAR LOCATION: CELL WALL BOUND.
-I- SUBCELLULAR LOCATION: CELL WALL BOUND.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institute modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A35066; A35066.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000209; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P00782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; J05229; AAA26960.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chen C.C., Cleary P.P.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=90153964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Streptococcus pyogenes. Bacteria; Firmicutes; B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
C5A PEPTIDASE PRECURSOR (EC 3.4.21.-) (SCP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SCPA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P15926;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SCPA_STRPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBTILASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KFKMWGAE 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 S08.020;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 62. 5; Conservative
1140
1158
130
193
512
1029
1034
1034
1051
1068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2SBT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
31
1167
1139
1157
1167
130
130
193
512
1104
1100
1050
1067
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed-2406246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73.3%;
62.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is not removed.
                                                                                 POTENTIAL.

CYTOPLASMIC (POTENTIAL).

CHARGE RELAY SYSTEM (BY SIMILARITY).

CELL WALL ATTACHMENT DOMAIN (POTENTIAL).

4 X 17 AA TANDEM REPEATS.
                                                                                                                                                                                                                                               C5A PEPTIDASE.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ã
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Usage
                                                                                                                                                                                                                                                                                                                      Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bγ
                                                                                                                                                                                                                                                                                                                  Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
```

```
ESULT 7
SBB_VIBCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
                                                                                                                            Matches
                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
  Q9KQU6;
01-OCT-2000
01-OCT-2000
                                                                                                                                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                      TRANSMEM CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P16808;
01-AUG-1990
01-AUG-1990
15-JUL-1998
                                                                                                                                                                                                  CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                          PIR; S09903;
PIR; S09759;
                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                              Chee M.S., Bankier A.T., Beck S., Bohni R., Brown C.M., Cerny R., Horsnell T., Hutchison C.A. III, Kouzarides T., Martignetti J.A., Preddie E., Satchwell S.C., Tomlinson P., Weston K.M., Barrell B.G.;
                                                                                                                                                                                                                                                                                                                                                                                                   Curr. Top. Microbiol. Immunol. 154:125-169(1990).
                                                                                                                                                                                                                                                                                                                                                                                                           "Analysis of the protein-coding content of the sequence cytomegalovirus strain AD169.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human cytomegalovirus (strain AD169).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Betaherpesvirinae; Cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-AUG-1990 (Rel. 15, Created)
01-AUG-1990 (Rel. 15, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL PROTEIN IRL10 PRECURSOR (TRL10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HCMVA
                               DSBB_VIBCH
                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                Hypothetical
                                                                                                                                                                                                                                                                                              EMBL;
                                                                                                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                              entities
                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
MEDLINE-90269039; PubMed-2161319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CBI_TaxID=10360;
                                                                                                                                                                                                                                                     IGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R10_HCMVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              473
                                                                                   78 YSAWGA 83
                                                                                                                                     Local
                                                                                              2 FSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RFSAWG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RFSSWG 478
                                                                                                                                                                                                                                                                                             X17403; CAA35300.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
5; Conserv
                                                                                                                           Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                             requires a license
  (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1127
                                                                                                                            Conservative
                                                                                                                                                                                                                                                                         S09903.
S09759.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                              protein;
                                                                                                                                                                                                   26
48
49
56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA; . 128263
 40,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1131
                                                                                                                                                                                                  171
171
100
48
49
56
                                                                                                                                   71.1%;
83.3%;
 Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73
                                                                                                                                                                                                                                                               Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . . .
...
...
...
                                                                                                                                                                              Œ;
  sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33; DB
Pred. No. 1.5e
1; Mismatches
                                                                                                                            ۲.
                                                                                                                                                                                                                                                                                                                            agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MΨ.
                                                                                                                                                                                                 N-LINKED
N-LINKED
                                                                                                                                  Score 32; DB
Pred: No. 36;
                                                                                                                                                                             N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
2C2E8AD869419B86 CRC64;
                                                                                                                                                                                                                              POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CONSERVED IN GRAM-POSITIVE COCCI SURFACE
                                                                                                                                                                                                                                          HYPOTHETICAL PROTEIN IRL10/TRL10.
                                                                                                                                                                                                                                                    POTENTIAL
                                PRT;
                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D2DDC52E5752DA5D CRC64;
                                                                                                                                                                                                                                                                                                                           removed. Usage by and for commercial ent (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                              Transmembrane; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          171
                                173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 1,
1.5e+02;
0;
                                                                                                                                                                                                                    (GLCNAC. .
                                                                                                                           0;
                                                                                                                                             Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 1167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                   (POTENTIAL)
                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                         restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                       of human
                                                                                                                                                                                                                                                                                                                                                                    EMBL
                                                                                                                                                                                                                                                                                                                                                                     a collaboration - MBL outstation
                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                    outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                          8
                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
  밁
                                                                                                                                                       Ş
                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                            Matches
                                                                                                                                                                                      Query Match
Best Local
                                        YEAST
YIV5_YEAST
P40579;
01-FEB-1995
01-FEB-1995
01-OCT-1996
                                                                                                                                                                                                                                        DISULFID DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DSBB
                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                          use
Saccharomyces cerevisiae (Baker's yeast).
                      SE
E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cholerae.
                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <del>-</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fraser C.M.;
                                                                                                                                                                                                                                                                         TRANSMEM
                                                                                                                                                                                                                                                                                             TRANSMEM
                                                                                                                                                                                                                                                                                                                   FRANSMEM
```

```
01-FEB-1995 (Rel. 31, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
HYPOTHETICAL OXIDOREDUCTASE IN LYS1-HYR1 INTERGENIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L., Bodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelln H., Richardson D., Ermolaeva M.D., Vamatheyan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleishmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE004266; AAF95050.1; TIGR; VC1902; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed. entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-EL TOR N16961 / SEROTYPE 01;
MEDLINE-20406833; PubMed-10952301;
Heidelberg J.F., Eisen J.A., Nelson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-0CT-2000 (Rel. 40, Last annotation update)
DISULFIDE BOND FORMATION PROTEIN B (DISULFIDE OXIDOREDUCTASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 406:477-483(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=666;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                               |:||||
77 FAAWGA 82
                                                                                                                                                                                                                                                                   2 FSAWGA 7
1. -. - . - ) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE DSBB FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. INNER MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PERIPLASMIC PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR VC1902
                                                                                                                                                                                                                                                                                                             Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         120
148
169
                                                                                  (Rel.
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15
36
51
72
                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REQUIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inner
                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Redox-active center;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                license agreement (See http://www.isb-sib
                                                                                                                                                                                                                                                                                                                                                                                                                 19334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14
50
71
98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           institutions as long
                                                                                                                                                                                                                                                                                                                              71.1%;
                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FOR DISULFIDE BOND FORMATION NS. ACTS BY OXIDIZING THE DSB.
                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gamma subdivision; Vibrionaceae; Vibrio
                                                                                                                                                                                                                                                                                                           Score 32; DB Pred. No. 36; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                  REDOX-ACTIVE (BY SIMILARITY).
REDOX-ACTIVE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PERIPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CYTOPLASMIC (POTENTIAL).
                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                 3B159DD2CA28D53B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Electron transport;
                                                                                                                           254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       There are no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                    Length 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DSBA
                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sellers P.,
                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (BY
                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        commercial
```

```
B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      岁
                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                  CAIB_ECOLI
P31572;
01-JUL-1993
01-FEB-1995
15-JUL-1998
L-CARNITINE
MEDLINE=92334977: PubMed=1630901;
Yura T., Mori H., Nagai H., Nagata T.,
Isono K., Mizobuchi K., Nakata A.;
                                                                            Eichler K., Schunck W.-H., Kleber H.-P., Mandrand-Berthelot "Cloning, nucleotide sequence, and expression of the Escheri gene encoding carnitine dehydratase.";
Bacteriol. 176:2970-2975(1994).
                                                                                                                                                                                                                                                                                                                              ECOLI
                                                                                                                                                SEQUENCE FROM N.A.,
STRAIN-044 K74;
                                                                                                                                                                                                   Bacteria; Proteobacteria;
Escherichia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A., Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M., Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D., Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V., Walsh S.V., Whitehead S., Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                          Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                 MEDLINE-94245624; PubMed-8188598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; 238061; CAA86195.1;
PIR; S48497; S48497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Appothetical protein; Oxidoreductase.
                                                                                                                                                                                                                                                                                                                                                                                    144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-S288C / AB972;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Fungi;
Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                          2 FSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P; P47227; 1BDB.
; S0001474; YIR035C.
erPro; IPR002198; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                 ||:|||
|FSSWGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150
254 AA;
                                                                                                                                                                                                                                                                 (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                   DEHYDRATASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                              26, Created)
31, Last sequence update)
36, Last annotation update)
RATASE (EC 4.2.1.89) (L-CDHT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                30 N
150 E
27480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                           AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                71.1%;
83.3%;
                                                                                                                                                                                                           gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                   1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAD OR NADP (BY SIMILARITY).
BY SIMILARITY.
; 916A5A460BE59F78 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB
Pred. No. 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                  405
             Ishihama A., Fujita
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                           DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ۲;
                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 254;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        no restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                a collaboration
                                                                                                                    Z
                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                       coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         its
                                                                                                                                                                                                                                                                                                                                                                                                                                0
```

```
RRA COC
                                                                                                                                                                                                                                                                                                                                        TOLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                 ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SET THE REPORT OF SECOND PROPERTY OF SECOND PROPERT
                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 5
                                                                                                                                                                                                  Q9Z7C4; Q9JQ31;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                          Chlamydia pneumoniae (Chlamydophila pneumoniae).
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydophila
                                                                                                                                                             TOLB PROTEIN PRECURSOR.
TOLB OR CPN0782 OR CP1090
                                                                                                                                                                                                                                                                                                                                     CHLPN
                 STRAIN-CWL029;
                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                             TOLB_CHLPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removentities requires a license agreement (some send an email to license@isb-sib.ch)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the En
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Lyase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- COFACTOR: AN UNKNOWN COFACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- CATALYTIC ACTIVITY: L-CARNITINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A
STRAIN=K12 / MG16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete genome sequence of Escherichia coliscience 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Systematic sequencing of the Escherichia the 0-2.4 min region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                 \frac{3}{3}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: CYTOPLASMIC.
INDUCTION: BY L-CARTNITINE OR CROTONOBETAINE.
SIMILARITY: TO BILE ACID-INDUCIBLE OPERON PROTEIN F (BAIF) FROM EUBACTERIUM SP. AND TO E.COLI YFDE.
                                                                                                                                                                                                                                                                                                                                                                                                                              |: ||||
FAEWGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAMMA-BUTYROBETAINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PATHWAY: CARNITINE METABOLISM. CONVERSION OF CARNITINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COFACTOR IS FOUND ONLY IN CELLS AND IN PRESENCE OF CARNITINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: CATALYZES THE ANAEROBIC DEHYDRATION OF L-CARNITINE (R-3-HYDROXY-4-AMINOBUTYRATE) TO CROTONOBETAINE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           X67748; CAA47971.1; -. X73904; CAA52112.1; -. D10483; BAA01314.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE000114; AAC73149.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EG11559; caiB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                405 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      S40559
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187
302
45126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20:3305-3308(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is not removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 32; DB Pred. No. 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> A (IN STRAIN (
-> A (IN STRAIN (
75583684B4B5A2DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IS NECESSARY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CROTONOBETAINE.
4-(TRIMETHYLAMMONIO)BUT-2-ENOATE
                                                                                                                                                                                                                                                                                                        431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N 044 K74).
N 044 K74).
DE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genome: analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FOR ACTIVITY
ANAEROBIC CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    restricti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CONDITIONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

MEDLINE=99206606; PubMed=10192388

```
HM1_PARDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                 01-OCT-1989
01-OCT-1989
15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for comparations
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi Shiba T., Ishii K., Hattori M., Ruhara S., Nakazawa T.; "Comparison of whole genome sequences of Chlamydia pneumoniae from Japan and CWL029 from USA."; Nucleic Acids Res. 28:2311-2314(2000).
SEQUENCE FROM
                                                                                    Bactería; Proteobactería;
                                                                                                                                                                               METHANOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F., White O., Hickey E.K., Peterson J., Umayam L.A., Utterback T., Berry K., Bass S., Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R., Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L., Elsen J., Fraser C.M.; "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.";
                                                                                                           Paracoccus denitrificans
                                                                                                                                                     ALPHA SUBUNIT) (MEDH).
                                                                                                                                                                                                                                                                     P12293;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-20330349; PubMed=10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-J138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Olinger L., Grimwood J., Davis R.V.
"Comparative genomes of Chlamydia
                                            NCBI_TaxID=266;
                                                                                                                                                                                                                                                                                            DHM1_PARDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ransport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic Acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20150255; PubMed=10684935;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kalman S., Mitchell W., Marathe R., Lammel C., Far
Olinger L., Grimwood J., Davis R.W., Stephens R.S.
                                                                                                                                                                                                                                                                                                                                                                                                     || :|||
415 RFPSWGA 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                             1 RFSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE TOLB FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: PERIPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genet. 21:385-389(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CP1090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AE001659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SIMILARITY)
                                                                                                                                                                        989 (Rel. 12, Created)
989 (Rel. 17, Last sequence update)
998 (Rel. 37, Last annotation update)
998 (Rel. 37, Last annotation update)
DEHYDROGENASE SUBUNIT 1 PRECURSOR (EC 1.1.99.8) (MDH LARGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3S-PROT entry is copyright. It is produced through a collaboration the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21
431 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Res. 28:1397-1406(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; AAD18920.1; -.
; AAF38861.1; -.
; BAA98990.1; -.
                                                                                                                                                                                                                                                                                          STANDARD;
  AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47761 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.18;
71.48;
SEQUENCE
                                                                                 alpha subdivision; Rhodobacter group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOLB PROTEIN.
D5AD80B32E563D1B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Periplasmic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
ę
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pneumoniae
  33-49
                                                                                                                                                                                                                                                                                          631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                          B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fan J., Hyman R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouchi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFFIFIER REPRESENTATION OF THE PROPERTY OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        __CORGL
CSP1_CORGL
Q01377;
Q1-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUL-1993
01-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DISULFID
DISULFID
ACT_SITE
SEQUENCE
deduced N-terminal region antigen 85 complex.";
Mol. Microbiol. 6:2349-236
-!- FUNCTION: ONE OF THE T
                                                                                                                                      Shechter E., Leblon G.;
"Cloning and nucleotide sequence of the cspl gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: the two major secreted proteins of Corynebacterium glutamicum: the contraction of the two major secreted proteins of Corynebacterium glutamicum: the contraction of the two major secreted proteins of Corynebacterium glutamicum: the contraction of the cspl gene encoding PS1, one of the two major secreted proteins of the cspl gene encoding PS1, one of the two major secreted proteins of the cspl gene encoding PS1, one of the two major secreted proteins of the cspl gene encoding PS1, one of the two major secreted proteins of the cspl gene encoding PS1, one of the two major secreted proteins of the cspl gene encoding PS1, one of the two major secreted proteins of corynebacterium glutamicum: the cspl gene encoding PS1, one of the two major secreted proteins of corynebacterium glutamicum: the cspl gene encoding PS1, one of the two major secreted proteins of corynebacterium glutamicum: the cspl general proteins of the cspl gen
                                                                                                                                                                                                                                                                             Joliff G.,
                                                                                                                                                                                                                                                                                                                       STRAIN-MELASSECOLA / ATCC 17965; MEDLINE-93023863; PubMed-1406274;
                                                                                                                                                                                                                                                                                                                                                             STRAIN-MELASSECOLA /
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacterium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF01011; Bacterial_PQQ; 7.
PROSITE; PS00363; BACTERIAL_PQQ_1;
PROSITE; PS00364; BACTERIAL_PQQ_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harms N., de Vries G.E., Maurer K., Hoogendijk J., "Isolation and nucleotide sequence of the methanol structural gene from Paracoccus denitrificans."; J. Bacteriol. 169:3969-3975(1987).

-i- CATALYTIC ACTIVITY: PRIMARY ALCOHOL + ACCEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS1 PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Oxidoreductase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M17339; AAA88366.1;
HSSP; P38539; 4AAH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001479;
InterPro; IPR002372;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=87307969; PubMed=3114231;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 RFSAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      European Bioinformatics Institute. The by non-profit institutions as long ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: PERIPLASMIC.
MISCELLANEOUS: MDH IS THE MAJOR PROTEIN IN THE CELL DURING ON METHANOL (IN P.DENITRIFICANS MDH CONSTITUTES UP TO 15% of the constitute of the constitution of the constit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE BACTERIAL POQ DEHYDROGENASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOTAL CELL PROTEIN).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFSVWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 5; Conserv
                                                                                                                                                                                                                                                                         Mathieu L., Hahn V., Bayan N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel.
(Rel.
(Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33
135
418
335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glutamicum (Brevibacterium flavum)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQQ;
                                          6:2349-2362(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26,
26,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       631
136
447
335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     69799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71.1%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal; Methanol utilization; Periplasmic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
                                                                                                             proteins of Corynebacterium of PS1 is similar to the Myc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BY SIMILARITY.
BY SIMILARITY.
BASE (POTENTIAL).
W; 0934DC93FFC5730B (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        METHANOL DEHYDROGENASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No. 1.2e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        There are no rest
                                                                                                                                                                                                                                                                             Duchiron F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CRC64;
                                                                                                             Mycobacterium:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        - ALDEHYDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Stouthamer A.H.; dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ьy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                             Renaud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for
                                                                                                                                                                                                                                                                             ĭ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                           the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

THE TWO MAJOR SECRETED PROTEINS

```
{}_{1} {}_{2} {}_{3} {}_{3} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {}_{6} {
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Juery Match
Best Local
                                                                                                                                         modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                 EMBL; X55995; CAA39468.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M2GD_RAT
Q63342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           clone.";
Eur. J. Biochem. 198:793-799(1991).
FI- CATALYTIC ACTIVITY: N,N-DIMETHYLGLYCINE + ACCEPTOR
FI- CATALYTIC ACTIVITY: N,N-DIMETHYLGLYCINE + ACCEPTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -1- COFACTOR: FAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
DIMETHYLGLYCINE DEHYDROGENASE, MITOCHONDRIAL PRECURSOR (EC 1.5.99.2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOD_RES
                                                                         nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-91266966; PubMed-1710985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ME2GLYDH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X66078; CAA46877.1;
PIR; S25184; S25184.
InterPro; IPR000801; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00756; Esterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | ||||:
| 609 FDAWGAK 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ignal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nepatocytes in
                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: MITOCHONDRIAL. SIMILARITY: BELONGS TO THE GCVT FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PATHWAY: CHOLINE METABOLISM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H., Polster M., Brandsch R.;

1iver dimethylglycine dehydrogenase. Flavinylation of the enzyme repatocytes in primary culture and characterization of a cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: SECRETED.
SIMILARITY: THE M-TERMINAL IS VERY SIMILAR TO THE COMPLETE SEQUENCES OF THE MYCOBACTERIAL ANTIGENS 85-A, 85-B & 85-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity 71., 5; Conservative
                                                                         IPR002536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   657 AA;
Flavoprotein; FAD; Mitochondrion; Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43
657
44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata;
Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70918 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               71.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1;
Pred. No. 1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PYRROLIDONE CARBOXYLIC ACID 5164B87626AC098F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PS1 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   857 · AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 657;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

D B

111 RYSDWGA 117

1 RFSAWGA 7

```
SALE ALL SALES AND ALL SALES A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
         Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                   Eye lens
                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRANSIT
CHAIN
BINDING
SEQUENCE
                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                           EMBL; M99583; AAA49694.1; -. HSSP; P02526; IGCS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
use by non-profit institutions as 1c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gene 128:189-195(1993).
-I- FUNCTION: CRYSTALLINS ARE THE DOMINANT STRUCTURAL COMPONENTS
                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -1- SUBUNIT: MONOMER (BY SIMILARITY).
-1- DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUVERY SIMILAR GREEK KEY MOTIFS.
-1- SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Smolich B.D., Tarkington S.K., Saha M.S., Stathakis D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAMMA CRYSTALLIN V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997 (Rel. 01-NOV-1997 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XENLA
                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Characterization of Xenopus laevis gamma-crystallin-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=93292986; PubMed=8514186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCRY5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CRG5_XENLA
Q06255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  717 FRAWGSE 723
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 FSAWGAE 8
                                                                                                                                                                                                                                                                        PF00030; crystall; 1.
TE; PS00225; CRYSTALLIN_BETAGAMMA;
                                                                                                                                                                                                                                                   protein; Duplication;
                                                                                                                                                                                                                                                                                                                         IPR001064; -
                                                                                                                    1
<1
42
46
87
132 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          857
         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 35, Created)
. 35, Last sequence. 35, Last annotation.
                                                                                                                                        41
45
86
132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35; Last sequence update)
35, Last annotation update)
(GAMMA-5-CRY) (FRAGMENT).
                                                                                                                      16461 MW;
                              68.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          71.18;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                          MOTIF 2.
CONNECTING PEPTIDE.
MOTIF 4.
WOTIF 4.
CBA97C33E2F75377 CRC64;
      1;
                           Score 31;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 32;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DIMETHYLGLYCINE DEHYDROGENASE FAD (COVALENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MITOCHONDRION (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                 Multigene
    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A6FED946B8AB9878 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no
                                                DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1.7e+02;
                                                                                                                                                                                                                                                 family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FOLDED INTO FOUR
    1;
                                              Length 132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 857
    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                      and
  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genes.";
Gaps.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                  commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ņ
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
```

```
Query Match
Best Local Similarity 100.
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REV_EIAV9
P11305;
01-JUL-1989
01-JUL-1989
01-FEB-1996
01-FEB-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE-87236196; PubMed-3035786;

KAWAKAMI T., Sherman L., Dahlberg J., Gazit A., Yaniv A.,

Kawakami T., Aaronson S.A.;

"Nucleotick S.R., Aaronson s.A.;

"Nucleotick sequence analysis of equine infectious anemia virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Equine infectious anemia virus (clone 1369) (EIAV).
Viruses; Retroid viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11670;
                                                                                                                                                                                                                                                                      Transcription regulation; Trans-acting factor; Activator; Nuclear protein.

1 1
                                                                                                                                                                                                                                                                                                                                                   EMBL; M16575; AAB59864.1; ALT_SEQ.
PIR; D27842; ASLJEW.
                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VIFOLOGY 158:300-312(1987).

1- FUNCTION: THE VAPPEARS TO ACT POST-TRANSCRIPTIONALLY TO RELIEVE NEGATIVE REPRESSION OF GAG AND ENV PRODUCTION.

1-1- SUBCELLULAR LOCATION: NUCLEAR PROTEIN THAT ACCUMULATES IN THE
                                                                                                                                                                                                                                             SEQUENCE
|||||
|100 FSAWG 104
                                                      2 FSAWG 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOLI.
                                                                                                                                                                                                                                             135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (Rel. 11, Created)
(Rel. 11, Last sequence update)
(Rel. 33, Last annotation update)
(3'-ORF PROTEIN) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                             15988 MW;
                                                                                                     68.9%; Score 31; DB 1; Length 135; 100.0%; Pred. No. 43; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                           8C56A9E96CD85DCD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         135 AA
                                                                                                             0;
                                                                                                          Gaps
                                                                                                                0
```

earch completed: October 18, 2001, 16:52:30 ob time: 115 sec

ţ.

```
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                   esult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             . num DB seq length: 0
איייישישים DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                        8
                                                                                                                                                                                                                                                                                                        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                       Score
                                                                                                                                                                                                                                                    Query
Match Length DB
       SPTREMBL_16:*
l: sp_archea:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        October 18, 2001, 16:50:35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      425026 seqs, 132305027 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-646-579-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                          sp_organelle:*
sp_phage:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_archea:*
sp_bacteria:*
                                                                                                                                                                                                                                                                                                                                                               sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sp_mammal:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_human: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sp_mhc: *
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   p_fungi:*
                                                                                                                                                                                                                                                                                                                                                                                                   sp_rodent:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         p_invertebrate:*
                                                                                                                                                                                                                                                                                                                                                                                                              sp_plant:*
     545
740
745
272
272
386
430
432
575
635
637
   Q9S3X4
Q9L629
) Q9FT16
1 Q69087
1 Q69104
Q44233
1 P89449
                                                                                                                 Q9UQQ1
L 054697
                                                                                                                                      Q9RRX3
) Q9FLE1
Q9V283
                                                                                                                                                                           P96264
Q9F2X2
Q9L270
Q9HZQ8
Q9KZN9
                                                                                                     Q9HX80
                                                                                          Q9RQ9.7
                                                                                                                                                                                                                                                                                         SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search time 33.31 Seconds (without alignments) 31.775 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               425026
        Q9v283 pyrococcus
Q9uqq1 homo sapien
O54697 rattus norv
Q9hx80 pseudomonas
Q9uq97 corynebacte
Q933x4 streptomyce
Q91629 streptomyce
Q91629 streptomyce
Q91616 oryza sativ
Q69087 human herpe
Q69104 herpes simp
Q44233 arthrobacte
                                                                                                                                                        P96264 mycobacteri
O9f2x2 streptomyce
O91270 streptomyce
O9hzq8 pseudomonas
O9kzn9 streptomyce
O9rx3 deinococcus
                                                                                                                                                                                                                                                Description
                                                                                                                                               Q9fle1 arabidopsis
P89449 herpes simp
```

ALIGNMENTS

QΥ

1 RFSAWGAE 8

1,

```
Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2000 (TIEMBLIEL 15, C
01-OCT-2000 (TIEMBLIEL 15, L
01-MAR-2001 (TIEMBLIEL 16, L
PUTATIVE SECRETED PROTEIN.
SCL2.29C.
                                                                                                                                                                STRAIN-A3(2);
Seeger K.J., Harris D.;
Submitted (JAN-2000) to
                                                                                                                                                                                                                                                                                                                                           Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St.

NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the 8 Mb Streptomyces coellcolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996). EMBL; AL392148; CAC08290.1; -.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Redenbach M., Kieser H.M., Denapaite D., Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed by the cosmids are considered by the cosmids and a detailed by the cosmids are cosmids are cosmids are cosmids and a detailed by the cosmids are cosmids are
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Streptomyces coelicolor.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Bactinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9L270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=A3(2);
Cerdeno A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saunders D.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
Cerdeno A.M., Parkhill J., E Submitted (JAN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97000351; PubMed=8843436;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (SEP-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PUTATIVE AMINOPEPTIDASE.
                                                                   STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aminopeptidase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 RFAWWGAE 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    309
                                                                                                       QUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ||: ||||
RFAFWGAE 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SEP-2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         324 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
Parkhill J., Ba מרכים
מחוץ to the F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Harris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         33594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     77.8%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
;
                                                                                                                                                                          the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
Barrell B.G., Rajandream M.A.;
e EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DB Pred. No. 80; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         53BB08E87F299389 CRC64,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eichner A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                          databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 324;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                           Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cullum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

```
RESULT
Q9KZN9
      3338U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ω
                                                                                                           ₽
                                                                                                                                å
                                                                                                                                                                                                                   밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [3]
SEQUENCE FROM N.A.
STRAIN=A3(2);
STRAIN=A7000351;
  01-OCT-2000
01-OCT-2000
01-MAR-2001
                                      Q9KZN9;
                                                                                                                                                                                                                                                                                                           Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P., Hilckey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M. Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y., Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M., Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000567; -. Pfam; PF01547; SBP_bact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97000351; PubMed-8843436;
Redenbach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                  Aminopeptidase.
SEQUENCE 536
                                                                                                                                                                                                                                     EMBL; AE004720; AAG06327.1; InterPro; IPR003137; -. Pfam; PF02225; PA; 1.
                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20437337; PubMed=10984043;
                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PAO1
                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9HZQ8;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99нг ов
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "A set of ordered cosmids and a detailed genetic and the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL137778; CAB70941.1;
                                                                                                                                                                                                                                                                            Nature 406:959-964(2000)
                                                                                                                                                                                                                                                                                        opportun
                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA2939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROBABLE AMINOPEPTIDASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pseudomonas
                                                                                                                                                                                                                                                                                                  "Complete genome sequence of Pseudomonas
                                                                                                          333 RFAWWGAE 340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               50 RYSWWGAE 57
                                                                                                                                 1 RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 RFSAWGAE 8
                                                                        G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6,
                                                                                                                                                                                                                                                                                      istic pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      433 AA; 47187 MW;
                                                                                                                                                                                                                  536 AA;
 (TrEMBLiel. (TrEMBLiel. (TrEMBLiel.
                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                 PRELIMINARY;
                                                                                                                                                                                                                  57511 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.8%;
75.0%;
                                                                                                                                                                 77.8%;
75.0%;
   16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gamma
Created)
Last sequence update)
Last annotation update)
                                                                                                                                                         <u>;</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
                                                                                                                                                                   Score 35; I
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB 2;
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; 1.
723846CF6CABC82E CRC64;
                                                                                                                                                                                                                  EE57BEFFC11C803A CRC64;
                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                        subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    536
                                                                                                                                                                   DB 2;
1.3e+02;
                                                 ₹
                                                                                                                                                                                                                                                                                                  aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eichner
                                                                                                                                                                             Length 536;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cullum
                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         0
```

ACETOACETYL-COA SYNTHETASE

Matches

5

Conservative

2

Mismatches

ļ

Indels

```
RESULT
29RRX3
ID Q
AC Q
DT 0
DT 0
DT 0
DT 0
DT 0
DT 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SON DE LE LA COMPANIE DE LA COMPANIE
                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  밁
  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local S
Matches 6
                                                                                                                                                                                                                                                   White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D., Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L., Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M., Vamathevan J.J., Lam P., McDonald L., Utterback T., Zalewski C., Makarova K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D. Ketchum K.A., Nelson K.E., Salzberg S., Smith H.O., Venter J.C.,
                                                                                                                                                          "Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.";
Science 286:1571-1577(1999).
                                                                                                                        EMBL; AE002066; AAF11904.1; TIGR; DR2359; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9RRX3;
01-MAY-2000
                                                                                                                                                                                                                                            Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=20036896; PubMed=10567266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Thermus/Deinococcus
NCBI_TaxID=1299;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONSERVED HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the 8 Mb Streptomyces coelicolor A3(2)
Mol. Microbiol. 21:77-96(1996).
EMBL; AL353861; CAB88889.1; -.
InterPro; IPR000873; -
PROSITE; PS00455; AMP_BINDING; 1.
SEQUENCE 658 AA; 72137 MW; 34AF9A24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-A3(2);
STRAIN-B97000351; PubMed-8843436;
MEDLINE-97000351; PubMed-8843436;
Denapaite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Deinococcus radiodurans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9RRX3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rican.
Streptomyces coelicolor.

nacteria: Firmicutes; Actinobacteria; Actinobacteridae;

nacteria: Firmicutes; Actinobacteria; Actinobacteridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          EQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bentley S.D., Parkhill J., J
Submitted (APR-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Actinomycetales;
NCBI_TaxID=1902;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A set of ordered cosmids and a detailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (APR-2000) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ۲
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REQAMAAE 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
6; Conser
                                                                                                  357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TremBurel. 13, Created)
(TremBurel. 13, Last sequence update)
(TremBurel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                             40102 MW;
    75
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 77.8%;
75.0%;
    . 5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Barrell B.G., Rajandream M.A.;
EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
  Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          group;
                                                                                             17A7D864C6184081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.
34AF9A24FF22F11D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
34;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Deinococcales; Deinococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D.,
DB 2;
1.3e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 2;
1.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 genetic and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eichner
                      Length 357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 658
                                                                                          CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physical map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cullum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
```

```
RESULT

ID

OPPLEI

OP
                                                                                                                  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Š
                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                             structure and evolution.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ
EMBL; AJ248283; CAB49115.1; ...
InterPro; IPR000567; ...
Pfam; PF01547; SBP_bacterial_1; 1.
SEQUENCE 545 AA; 61787 MW; 6ED118EE38FB5C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               [1]
SEQUENCE FROM N.A.
STRAIN-COLUMBIA;
MEDLINE-98290546; Pubmed-9628582;
MEDLINE-98290546; Notani H., Na
                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. STRAIN=ORSAY;
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
SUGAR ABC TRANSPORTER BI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                           Archaea; Euryarchaeota;
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                      Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                                                                                  PAB2439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9V283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9V283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome Sequence features of the regions of 1,456,315 bp covered physically assigned Pl and TAC clones.";
DNA Res. 5:41-54(1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress)
Eukaryota; Viridiplantae; Embryophyta;
Magnoliophyta; eudicotyledons; core eu
                                                                                                                                                                                                                                           Pyrococcus abyssi genome sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tabata S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassicales; Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FLE1;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENOMIC DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9FLE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 RFSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               α
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RLSAWGA 301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESAWGAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RFNAWGGK 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB010077; BA
VCE 454 AA;
      Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TIEMBLIE1. 16, Created)
(TIEMBLIE1. 16, Last sequence update)
(TIEMBLIE1. 16, Last annotation update)
, CHROMOSOME 5, P1 CLONE:MYH19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           œ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAB10218.1; -
AA; 48839 MW;
                         75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.6%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  BINDING
                                                                                                                                                                                                                                                                                                                                                                           Thermococcales; Thermococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracnecdons; core eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis.
Score 34; DB
Pred. No. 2.1e
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 34; DB
Pred. No. 1.7e
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                         1.
6ED118EE38FB5C34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EF503DA88D24F730 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nakamura Y.,
                                                                                                                                                                                                                                           insights into archaeal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             545
2.1e+02;
ches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                           tation update)
RELATED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 10; 1
1.7e+02;
thes 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tracheophyta;
                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ĀĀ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asamizu E.,
                                                                                                                                                                                                  databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosidae;
                                         Length 545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           covered by nineteen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; e; eurosids II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .
.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

Š

Matches

Conservative

2;

Indels

0;

Gaps

0

Qy

2 FSAWGAE

æ

```
ESULT
9UQQ1
Query Match
Best Local Similarity
Matches 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                           STRAIN-SPRAGUE-DAWLEY; TISSUE-ILEUM; shneider B.L., Thevananther S., Moyer M.S., Devarajan P., Sun A.Q., Dawson P.A., Ananth J. Biol. Chem. 0:0-0(1997).

EMBL; AP009921; AAB87644.1; -.
MEROPS; M28.011; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
SEQUENCE
                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               with N-acetylated alpha-linked peptidase IV activity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-SMALL INTESTINE;
MEDLINE-99185063; PubMed-10085079;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                      SEQUENCE
                                                                                           InterPro; IPR003137; -.
                                                                                                                                                                                                                         NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                               01-OCT-2000
                                                                                                                                                                                                                                                                                                         01-JUN-1998
01-JUN-1998
                                                                                                                                                                                                                                                                                                                                        054697;
                                                                                                                                                                                                                                                                                                                                                      054697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ012371; CAB39968.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pangalos M.N., Neefs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAALADASE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAALADASE L PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Isolation and expression of novel human glutamate
                                                                                                                                                                                                                                                                                                                                                                                                                        410 FASWGAE 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63
                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 FSAWGAE 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B101.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KFSAWGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PTO; IPR003137; -.
PTO2225; PA; 1.
TE; PS00107; PROTEIN KINASE_ATP; UNKNOWN_1.
NCE 740 AA; 80620 MW; E2E5AAC9E5056A14 CRC64;
                                                                                   PF02225;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chem. 274:8470-8483(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (TrEMBLrel.) (TrEMBLrel.)
                                                                      745
                                                                                                                                                                                                                                                                                            (TrEMBLrel.
                                                                                                                                                                                                                                                                                                         (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
 Conservative
                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          69
                                                                    PA;
                                                                    1.
80640 MW;
          75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.6%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13,
15,
                                                                                                                                                                                                                                                                                            15,
06,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Somers
                                                                                                                                                                                                                                                                                           Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 34; DB Pred. No. 2.8e 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2;
Score 34; DB 11;
Pred. No. 2.8e+02;
2; Mismatches (
                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                    A59C2EFD23BE36B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acidic
                                                                                                                                                      c M.S., Walters H.C., Ananthanarayanan M.;
                                                                                                                                                                                                                                                                                                                                                   745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fraiponts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               dipeptidase and dipeptidyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        лв ч,
2.8e+02;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 4;
                                                                                                                                                                                                                                                                                                                                                   ₹
                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 740
                          Length 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      E .
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            carboxypeptidases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ashton
                                                                                                                                                                                                                                      Murinae; Rattus
                                                                                                                                                                    Rinaldo
0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
```

```
Q9RQ97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
Q9HX80
                                                                                                                                                                                                                                                                                                                                                                                                          밁
                                                                                                                                                                                                                                                                                                                                                                                                                                QY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  В
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
                                                                                                                                                                                                                                                                                            Q9RQ97;
Q9RQ97;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-20437337; PubMed-10984043;
Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P. Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y. Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M. Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                          pathway: isolation and analy synthase.";
Mol. Cells 9:300-308(1999).
EMBL; AF126955; AAD54070.1;
InterPro; IPR000277; -.
                                                                                                                                                                                                                        Corynebacterium glutamicum (Brevibacterium flavum)
Bacteria; Firmicutes; Actinobacteria; Actinobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complete genome sequence of Pseudomonas aeruginosa PA01, popurtunistic pathogen."; Nature 406:959-964(2000).
EMBL; AE004811; AAG07323.1; -.
  SEQUENCE
                 Pfam;
                                                                                               Hwang B.J., Klm Y., Kim H.B., Hwang H.J., Kim J.H., Lee H.S.;
"Analysis of corynebacterium glutamicum methionine biosynthetic
                                                                                                                                         STRAIN-ASO19
                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                               Actinomycetales; Corynebacterineae; Corynebacterium.
                                                                                                                                                                                                                                                      METB.
                                                                                                                                                                                                                                                                CYSTATHIONINE
                                                                                                                                                                                                                                                                                  01-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00528; BPD_transp; 1. SEQUENCE 272 AA; 29447 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-PAOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ol-MAR-2001 (TrEMBLrel. 16, Created)
Ol-MAR-2001 (TrEMBLrel. 16, Last sequence upol-MAR-2001 (TrEMBLrel. 16, Last annotation upol-MAR-2001 (TrEMBLR) and TAURINE TRANSPORTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9HX80;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08XH6Ö
                                                                                                                           MEDLINE-99347339; PubMed-10420990;
                                                                                                                                                                                NCBI_TaxID=1718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PA3936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                        267 RFAAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 RFSAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FASWGAE 421
                                                                                                                                                                                                                                                                                                                                                                                                                                                              similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000515; -.
53; Cys_Met_Meta_PP; 386 AA; 41658 MW;
                                                                                                                                                                                                                                                                (TIEMBLIE1. 13, Created)
(TIEMBLIE1. 13, Last sequence update)
(TIEMBLIE1. 14, Last annotation update)
NE GAMMA-SYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                          272
                                                                                                                                                                                                                                                                                                                                                                                                                                   σ
                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                 and analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%;
83.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 33; DB 2;
Pred. No. 1.5e+02;
                                                                                                                                                                                                                                                                                                                                      PRT;
 72EBB2B34275296A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  D64898B300B2D06F CRC64;
                                                                                 of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                  metB
                                                                                                                                                                                                            Corynebacteriaceae;
                                                                                                                                                                                                                                                                                                                                      386
                                                                                                                                                                                                                         Actinobacteridae;
                                                                                 encoding cystathionine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 272;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lim R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                               gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
```

밁 Ş

118 FTAWGVE 124

2 FSAWGAE 8

Query Match
Best Local Similarity
Straightful Straight

Conservative

1;

Mismatches

2.2e+02; 1; DB 2;

Indels

0;

Gaps

0;

2

RFSAWGA

7

Length 386

73.3%;

Score 33; Pred. No.

```
RESULT
Q9S3X4
ID Q99
AC Q99
DT 011
DT 011
DT 011
DT SPC
GN SPC
OS St
                                                                         용
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SORET REPRESE
    Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                 01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                  *Cloning and Identification of a Gene Cluster spectabilis Spectinomycin Producer."; Submitted (MAR-2000) to the EMBL; GenBank/DDBJ EMBL; AF244574; AAF63340.1; -SEQUENCE 432 AA; 45316 MW; 99B4FC1B822EBBC
                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-ATCC27741;
Sohng J.K., Kim S.B.,
Suh J.W.;
                                                                                                                                                                                                                                                                                                                                        Q9L629
Q9L629;
                                                                                                                                                                                                            Streptomyces spectabilis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.

MCBI_TaxID=68270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Altenbuchner J., Jennen D., Volff J.N.;
"The spectinomycin resistance gene of the spectinomycin producer Streptomyces spectabilis.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF170704; AAD50454.1;
SEQUENCE 430 AA; 44966 MW; 91DF225A21906AAA CRC64;
                                                                                                                                                                                                                                                                                    EXPORT PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-NRRL 2494;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Streptomyces spectabilis.

Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycesae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9S3X4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q9S3X4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=68270;
                                                                                                                                                                                                                                                                                                                                                                                                                            367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity 71.4 hes 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 RFSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                          RFAVWGA 373
    Similarity 71.4
5; Conservative
                                                                                                                                                                                                                                                                                            (TremBLrel. 15, Created)
(TremBLrel. 15, Last seq
(TremBLrel. 15, Last ann
                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
               73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73.3%;
                                                                                                                                                    Cha J.H., Hahn J.J., Kim J.W., Hyun C.G.,
 Score 33; DB 2;
Pred. No. 2.5e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 33; DB 2;
Pred. No. 2.5e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                     99B4FC1B822EBBC0
                                                                                                                                                                                                                                                                                                                                                    432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   430 AA
  1;
                                                                                                databases
                                                                                                                         in Streptomyces
                           Length 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 430
  Indels
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
 Gaps
0
```

```
망
                                                                                            Ş
Search completed: October 18, 2001, 16:53:10 Job time: 155 sec
                                                                                                                                                                                       RESULT
Q9FTI6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
                                                                                                                    Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9FTI6;
                                                                                                                                                                                     STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamamoto K.;
Sasaki T., Matsumoto T., Yamamoto DNA, Chromosome
"Oryza sativa nipponbare(GA3) genomic DNA, Chromosome
clone:P0410E01.";
clone:P0410E01.";
submitted (SEP-2000) to the EMBL/GenBank/DDBJ database.
SEMBL, AP002866; Babil7093.1;
SEQUENCE 575 AA; 60463 MW; D100FB76F4A4C134 CRC64;
                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae; I
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             oryza
                                                                                                                                                                                                                                                                                                                                                                              P0410E01.14 PROTEIN.
P0410E01.14.
                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4530;
                                                                 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                369
                                                                                1 RFSAWGA 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15
                                                                 RFAGWGA 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              II: III
RFAVWGA 375
                                                                                                                    Similarity
5; Conserv
                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                17093.1; -.
60463 MW; D100FB76F4A4Cl34 CRC64;
                                                                                                                                 73.3%;
71.4%;
                                                                                                                                                                                                                                                                                                                                  Embryophyta; Tracheophyta; Spermatophyta; Poales; Poaceae; Ehrhartoideae; Oryzeae;
                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                Score 33; DB 10;
Pred. No. 3.3e+02;
1; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           575
                                                                                                                                                                                                                                                                                                                                                                                                                                                           ₽
                                                                                                                                         Length 575;
                                                                                                                                                                                                                                      1,
                                                                                                                 0;
                                                                                                                Gaps
                                                                                                                0;
```

```
Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POST-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mum DB seq length: 0 mum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 18, 2001, 16:51:16; Search time 32.41 Seconds (without alignments) 16.835 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A_Geneseq_0601:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412676 seqs, 60623988 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BLOSUM62 . Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-09-646-579-2
49
/SIDSB/gcgdata/geneseq/geneseqp/AA1993.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1994.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1995.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1997.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1999.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA1990.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA2000.DAT:*
/SIDSB/gcgdata/geneseq/geneseqp/AA2001.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                   /SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:
                                                                                                                                                                                                                                                                                                                                                 /SIDS8/gcgdata/geneseq/geneseqp/AA1988.DAT;*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'SIDS8/gcgdata/geneseq/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                     SIDS8,
                                                                                                                                                                                                                                                                                                                                                                                                                                     SIDS8,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:
                                                                                                                                                                                                                                        /SIDS8/gcgdata/geneseq/geneseqp/AA1991.DAT:*
/SIDS8/gcgdata/geneseq/geneseqp/AA1992.DAT:*
                                                                                                                                                                                                                                                                                           /SIDS8/gcgdata/geneseq/geneseqp/AA1990.DAT:*
                                                                                                                                                                                                                                                                                                                                                                          /gcgdata/geneseq/geneseqp/AA1986.DAT:*
/gcgdata/geneseq/geneseqp/AA1987.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                             /gcgdata/geneseq/geneseqp/AA1985.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gcgdata/geneseq/
                                                                                                                                                                                                                                                                                                                      gcgdata/geneseq/geneseqp/AA1989.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /geneseqp/AA1982.DAT:*
/geneseqp/AA1983.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        412676
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

;	11		οα	, ~	ισ	٠ u	4.0	. (.		, <u>–</u>	No.	000
Ü	3 7		ı (J	ı ü	ı ü) L) ()	ω U	49	49	Score	
11.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	71.4	100.0	100.0	Match	*
20	200	19	19	13	12	11	10	9	9	9	Match Length DB	
1/	17	18	17	20	20	15	15	15	20	19	DB	
AAR95344	AAR95394	AAW43951	AAR95345	AAW94964	AAY27077	AAR61960	AAR61951	AAR61853	AAY42322	AAW56752	ID	
MBP-3 (111-130).	Residues 101-120 o	Human myelin basic	MBP-3.1 (111-129)	MHC binding pepti	Myelin basic prote	MBP peptide 108.	MBP peptide 110.	MBP peptide 110.	Acinetobacter-deri	A. calcoacetions	Description	

ny cana	AAW06103	17	373	71.4	35	Ġ
mvelin bac	AAW06108	17	203	71.4	35	4
myeli	AAW06107	17	203	71.4	35	ũ
mvelin	AAY95922	21	197	71.4	35	Z
	AAW00399	17	197	71.4	ω	, <u>-</u>
mvelin	AAY44234	21	171	71.4	35	Ö
acid se	AAY69394	21	171	71.4	ω 5	9
mvelin	AAB19513	21	171	71.4	35	8
mvelin	AAY27284	20	171	71.4	ယ	37
myelin bas	AAR99580	17	171	71.4	ω 5	6
Human myelin basic	AAR97627	17	171	71.4	35	Ğ
ian generic	AAY58368	21	170	71.4	35	34
basic	AAW57236	19	170	71.4	. 35	ω
basic	AAR86422	17	170	71.4	35	32
Myelin oligodendro	AAR95406	17	170	71.4	35	31
	AAR48592	15	170	71.4	35	Ö
basic	AAR45947	15	170	71.4	35	29
basic	AAR35440	14	170	71.4	ω G	8 2
~	AAR30736	14	170	71.4	35	27
DICEO	AAR30735	14	170	71.4	35	26
hacio	AAR02226	11	170		35	25
בי בי בי	AAR48593	15	169		35	24
Rabbit muelin basi	AAR48594	15	168	71.4	35	23
Finition of the following states of the stat	AAR04717	=	168	71.4	35	22
Part of	AAR48595	15	167	71.4	35	21
minglis basis	AAR48596	15	127	71.4	ω 5	20
(FOR FOO!	AAW43953	18	25	71.4	35	19
$\overline{}$	AAR95347	17	25	71.4	35	18
a	AAR95367	17	25	71.4	35	17
N I	AAY85551	21	20	71.4	35	16
Human myelin basic	AAB12619	21	20	71.4	35	15
myelin	AAW73618	20	20	71.4	35	14
myo) in	6	18	20	71.4	35	13
ה מ	AAW4 3950	18	20	71.4	35	12

ALIGNMENTS

```
RESULT
                                                                              AAW56752
31-JUL-1998 (first entry)
                                                        AAW56752 standard; peptide; 9 AA.
                                  AAW56752;
```

A. calcoaceticus antigenic peptide exhibiting molecular mimicry

BSE; bovine; myelin; molecular mimicry; antigenic; assay; diagnusis; spongiform encephalopathy; Creuzfeld Jacob disease; multiple sclerosis; Acinetobacter calcoaceticus; Agrobacterium; Ruminococcus.

X X X X

Acinetobacter calcoaceticus

WO9813694-A1

02-APR-1998.

29-SEP-1997; 97WO-GB02667.

27-SEP-1996; 96GB-0020195

(UNLO) KING'S COLLEGE

Ebringer A;

WPI; 1998-230844/20

Diagnosis of demyelinating conditions, particularly BSE - by assaying for antibodies which bind to an antigenic peptide which exhibits molecular mimicry of a mammalian myelin peptide

ស៊ីនិស័ស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ីស៊ី

```
ESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bovine SE (BSE) in cattle comprises assaying sera collected from the cattle for antibodies to a species of Acinetobacter, Agrobacterium or Ruminococcus, or a peptide having a sequence present in the species which mimics a peptide of bovine myelin and identifying animals having a level of antibodies at least 2 standard deviations above that of healthy control animals. The diagnostic test kit for BSE in cattle comprises as test antigen a species of Acinetobacter, Ruminococcus or Agrobacterium or a peptide having a sequence present. In the species which mimics a peptide of bovine myelin. The methods can be used for diagnosis of demyelinating conditions such as BSE, Creuzfeld Jacob disease and multiple sclerosis.
This sequence represents a synthetic peptide epitope (#2) derived from species of Acinetobacter, which is sufficiently conformationally similar to natural Acinetobacter peptide epitopes to bind the corresponding antibodies. Acinetobacter species may be implicated in spongiform encephalopathies such as Creutzfeldt-Jakob disease or in de-myelinating diseases such as multiple sclerosis. Involvement of Acinetobacter forms the basis for a model for the development of de-myelinating diseases (an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This is a Acinetobacter calcoaceticus antigenic peptide that exhibits molecular mimicry to a bovine myelin peptide. This is used in the method and diagnostic tests for spongiform encephalopathy (SE) and other demyelinating conditions in mammals which comprises assaying antibodies present in the mammal which bind to an antigenic peptide which exhibits molecular mimicry of a mammalian myelin peptide. A method for testing for the mammalian myelin peptide.
                                                                                                                                                                                                                                                     Claim 12; Page 7; 11pp; English
                                                                                                                                                                                                                                                                                                                   Detecting de-myelinating disease or spongiform encephalopathy
                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-571874/48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         19-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09947932-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acinetobacter; myelin; spongiform encephalopathy; CJD; in Creutzfeldt-Jakob disease; multiple sclerosis; antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter-derived peptide epitope #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY42322;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY42322 standard; peptide; 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UNIO ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LONDON KING'S COLLEGE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7; 12pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98GB-0005913.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-GB00876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 49; DB 19;
Pred. No. 3.4e+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                immune response;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the methods
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                         similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0
```

(and

AAR61714-837 are potential peptide binders of peptides are thus potentially immunogenic. The using an algorithm, which assigns a score for

of HLA-A2.1 They were pa

motif.

each amino acid,

autoimmune diseases.

Page 122;

138pp; English.

Immunogenic peptide(s) having for treatment or prophylaxis

g an HLA-A2.1 binding motif - of cancer, virus infection or

ç

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR61853
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                           05-MAR-1993;
04-JUN-1993;
29-NOV-1993;
                                                                                                                                                                    Grey
                                                                                                                                                                                                                                                                                                                                                                                                              makes-1; melanoma antigen-1; core antigen; surface antigen; pharmaceutical composition; in vivo; ex vivo; therapeutic; diagnostic; MHC class I molecule; major histocompatability complex; HLA-A2 1; 9mer; 10mer; anchor; human lemkocuto antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           exposed to certain bacteria containing peptide sequences which mimic myelin peptides, experience an autoimmune response. A novel method for detecting a de-myelinating disease or spongiform encephalopathy in mammals has been developed which comprises testing a biological sample
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     obtained from the mammal for immunoglobulin A (19A) antibodies indicative of infection by Acinetobacter species. This sequence can be used as a test antigen in a kit to detect such antibodies. The method is useful for diagnosing de myelinating diseases and spongiform encephalopathies in
                                                                                                                                         WPI; 1994-302678/37.
                                                                                                                                                                                                                                                                                                                                            WO9420127-A.
                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                 algorithm prediction; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR61853;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           animals and humans, especially bovine spongiform encephalopathy, multisclerosis or Creutzfeldt-Jacob disease in humans. The method is useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     an alternative model for the development of spongiform encephalopathies) This model involves the phenomenon of molecular mimicry in which mammals
                                                                                                                                                                                                (CYTE-)
                                                                                                                                                                                                                                                                                     04-MAR-1994;
                                                                                                                                                                                                                                                                                                                15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR61853 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              for the early detection of these infections,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 isrfawgev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISRFAWGEV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peptide 110, potential binder of HLA-A2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     en; epitope; immunogenic target protein; PSA; HBVc; plasma specific antigen; hepatitis B virus; Epstein immunodeficiency virus; human papilloma virus; p53;
                                                                                                                                                                                                CYTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                           93US-0027146.
93US-0073205.
93US-0159184.
                                                                                                                                                                   ¥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                   94WO-US02353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                      Sette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                   ?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 49; DB zu;
Pred. No. 3.4e+05;
                                                                                                                                                                   Sidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              resulting in early
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indeis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       c-ERB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         multiple
```

0

0;

0;

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A-061951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           გვგვგვგვვ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
AAR61714-837 are potential peptide binders of HIA-A2.1 motif. These peptides are thus potentially immunogenic. They were predicted by using an algorithm, which assigns a score for each amino acid, at each position along a peptide. A peptide is scored in the 'Grouped Ratio' algorithm as a product of the scores of each of its residues. This peptide has an algorithm score (EO2) of -28.98. This value can then be used to predict a population of peptides with the highest occurrence of good binders. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can
                                                                                                                                                                                                                                                                                                                                             05-MAR-1993;
04-JUN-1993;
29-NOV-1993;
                                                                                                                                                        Disclosure; Page 128; 138pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antigen; epitope; immunogenic target protein; PSA; HBVC; HBVS; EBV; HIV1; plasma specific antigen; hepatitis B virus; Epstein Barr; human immunodeficiency virus; human papilloma virus; p53; c-ERB2;
                                                                                                                                                                                                    Immunogenic peptide(s) having for treatment or prophylaxis c
                                                                                                                                                                                                                                                                                                                                                                                                         04-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9420127-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAGE-1; melanoma antigen-1;
pharmaceutical composition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR61951;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR61951 standard;
                                                                                                                                                                                                                                                                                                               (CYTE-) CYTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                     15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        diagnostic; MHC class I molecule; major histocompatabil.
HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MBP peptide 110, potential
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          each position along a peptide. A peptide is scored in the 'Grouped Ratio' algorithm as a product of the scores of each of its residues. This peptide has an algorithm (EO2) of -21.42. This value can then be used to predict a population of peptides with the highest occurrence of good binders. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               be used for the treatment or prophlyaxis of cancer,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N
                                                                                                                                                                                                                                                                                   , MH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              l Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    or lymphoma,
                                                                                                                                                                                                                                                                                 Kast WM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               prediction;
                                                                                                                                                                                           diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      æ
                                                                                                                                                                                                                                                                                                               CORP.
                                                                                                                                                                                                                                                                                                                                           93US-0027146.
93US-0073205.
93US-0159184.
                                                                                                                                                                                                                                                                                                                                                                                                       94WO-US02353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide; 10 AA.
                                                                                                                                                                                                                                                                                Sette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MBP
                                                                                                                                                                                                                                                                                ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binder of HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     in vivo; ex vivo; therapeutic; ecule; major histocompatability complex;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      core antigen; surface antigen;
                                                                                                                                                                                                      g an HLA-A2.1 binding of cancer, virus info
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35;
Pred. No.
                                                                                                                                                                                                                                                                              Sidney
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 15;
                                                                                                                                                                                                      .1 binding motif - used virus infection or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                eg. prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
```

```
ďď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Them 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SXSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAR61960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
                            AAR61714-837 are potential peptide binders of HLA-A2.1 motif. These peptides are thus potentially immunogenic. They were predicted by using an algorithm, which assigns a score for each amino acid, at each position along a peptide. A peptide is scored in the 'Grouped Ratio' algorithm as a product of the scores of each of its residues. This value can then be used to predict a population of peptides with the highest occurrence of good binders. The peptides of the invention can induce cytotoxic T lymphocytes which can react with target cells. They can be used for the treatment or prophlyaxis of cancer, eg.
                                                                                                                                                                                                                                                                                                                                  05-MAR-1993;
04-JUN-1993;
29-NOV-1993;
                        prostate
                                                                                                                                                                    Disclosure; Page 129; 138pp; English
                                                                                                                                                                                                autoimmune
                                                                                                                                                                                                       Immunogenic peptide(s) having an HLA-A2.1 binding motif - used for treatment or prophylaxis of cancer, virus infection or
                                                                                                                                                                                                                                                   WPI; 1994-302678/37.
                                                                                                                                                                                                                                                                              Grey HM,
                                                                                                                                                                                                                                                                                                                                                                                      04-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                           W09420127-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           algorithm prediction; MBP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            be used
cancer o
                                                                                                                                                                                                                                                                                                        (CYTE-)
                                                                                                                                                                                                                                                                                                                                                                                                                 15-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pharmaceutical composition; in vivo; ex vivo; therapeutic;
diagnostic; MHC class I molecule; major histocompatability complex;
HLA-A2.1; 9mer; 10mer; anchor; human leukocyte antigen; PLP; 8mer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MBP peptide 108, potential binder of HLA-A2.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIV1; plasma specific antigen; hepatitis B virus; Ep
human immunodeficiency virus; human papilloma virus;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR61960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR61960 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAGE-1; melanoma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ŋ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||:||
!srfswg
                                                                                                                                                                                                                                                                                                        CYTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              o
H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       for the treatment
                       cancer or lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epitope; immunogenic target protein;
                                                                                                                                                                                                                                                                            Kast WM,
                                                                                                                                                                                               ent or prophylaxis diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                æ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                              9305-0159184
                                                                                                                                                                                                                                                                                                                                              93US-0027146
93US-0073205
                                                                                                                                                                                                                                                                                                                                                                                     94WO-US02353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antigen-1; core antigen; surface antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                              Sette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.48;
71.48;
                                                                                                                                                                                                                                                                            A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             11
                       etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                                                                                                                                                                                                                                           Sidney J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       prophlyaxis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of cancer, eg prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Epstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HBVc;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          p53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HBVs;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         :c-ERB2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
```

Query Match

71.48;

Score

35; DB

15;

Length 11;

Sequence

11

AA;

```
ESULT
AW94964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ĕ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ¥
                                                                                                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 71,4%;
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The invention relates to a method for treating inflammatory arthritis by administering antiarthritic peptides comprising an amino acid residue sequence that is identical to or homologous to a contiguous stretch of at least 10 amino acids of sequences shown in AAY27077 and AAY27078 (residues 110-121 or 153-162 of myelin basic protein (MBP)). The new method is useful for treating inflammatory arthritis in a mammal,
    12-MAY-1999
                                        AAW94964;
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                         especially a dog, horse or human, and for preventing the onset of arthritis. The peptides are useful as antiarthritic vaccines. The method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-493521/41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           22-OCT-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-AUG-1999.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US5942491-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sus sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Myelin basic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY27077 standard; peptide; 12 AA.
                                                                        AAW94964 standard; peptide; 13 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                             specifically uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Column 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Treating inflammatory arthritis using peptides with homology to known proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Root-Bernstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UNMS ) UNIV MICHIGAN STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY27077;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inflammatory arthritis; antiarthritic; myelin basic protein; MBP;
                                                                                                                                                                                                                                                                                                                                                                                                         nflammatory arthritis.
                                                                                                                                                                                                                                                    Local Similarity
nes 5; Conserv
                                                                                                                                                                                                            1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      lsrfswg 10
                                                                                                                                                                                                                                                                                                                                                 12
                                                                                                                                                                                                                                                    Conservative
(first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       96US-0735253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96US-0735253
                                                                                                                                                                                                                                                                                                                                                                                                       peptide sequences shown in AAY27085-92 for treating ritis. The present sequence represents a MBP peptide
                                                                                                                                                                                                                                                                    71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MBP) fragment (residues 110-121).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2;
                                                                                                                                                                                                                                                                  Score 35; D
Pred. No. 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred. No. 2.8;
2; Mismatches
                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                       DВ
                                                                                                                                                                                                                                                                                       20;
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                       Length 12;
                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
```

EEXEXEX

16-DEC-1996 AAR95345;

(first entry)

MBP-3.1 (111-129).

Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; CD4+; T-cell; autoimmune disease; demyelination; central nervous system;

문 Q

Query Match
Best Local Similarity
Matches 5; Conserv

Conservative

2;

71.48; 71.48;

Score 35; Pred. No. Mismatches

DB 3.3; 20; 0;

Length 13; Indels

0,

Gaps

RESULT

80

AAR95345 standard; peptide; 19

```
PD
                                                                                                                                                                                                  MIC molecule unitarily grove, (w) presenting a mic molecule and ascertaining a first conformation score for each pocket bound peptide side-chain; (c) amending the conformation of each pocket bound peptide side-chain and ascertaining a second conformation score; (d) repeating (c) with alternative conformations of each peptide pocket bound side-chain; (e) choosing the highest conformation score for each pocket bound peptide side-chain in each binding groove pockets, and (f) combining the highest conformation score for each pocket and ascertaining a binding score for the complete peptide. The invention als provides a computer conditioned to receive information characterising a
                                                                  peptide bound to the MHC molecule and to utilise the information to predict the binding affinity of the peptide. The method can be used to identify peptides in a protein which can bind to a given MHC molecule. Such peptides can be used in the production of molecules for use in e.g vaccines, autoimmune diseases and diagnostics. Sequences AAW94957 to AAW94981 represent peptides from myelin basic protein (MBP) that can bi
                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a method for the prediction of the binding affinity of a peptide to major histocompatibility (MHC) class II molecules. The method comprises (a) ascertaining the characteristics of a MHC molecule binding groove; (b) presenting a selected peptide to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying MHC binding peptides - by ascertaining the characteristics of a MHC molecule binding groove and determining conformation scores of pocket bound peptides
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brooks T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       W09859244-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Major histocompatibility class II; MHC; binding; vaccine; MBP; autoimmune disease; myelin basic protein; HLA-DRB1*0401.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MHC binding peptide from myelin basic protein (MBP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Example 4; Page 50; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-105639/09.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (ECLA-) ECLAGEN LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20-JUN-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1998;
                                                 molecule HLA-DRB1*0401.
    13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Carr F,
    Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           97GB-0012892
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98WO-GB01801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fothergill J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kemp
                                                                                                                                                                                                                                       The invention also
                                                                                                tor use in e.g.
AAW94957 to
                                                                       that can bind
```

myelin autoantigen; I

PLP;

```
RESULT
AAW43951
                                                                                                                                                                                                        무
                                                                                                                                                                                                                                                                                                                                                sclerosis (MS). These sequences can be used in compositions for treating MS in a mammal. The composition acts to down regulate the autoimmune response, and may be administered in an amount sufficient to prevent the onset of symptoms of MS. The compositions may also be used to treat advanced stage MS, especially relapsing-remitting MS, chronic treat advanced stage MS. These peptides may also be used in the treatment of other diseases involving myelin autoantigens, including diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and rheumatoid arthritis. Peptides derived from other myelin autoantigens, such as myelin oligodendrocyte protein (MGG), proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can be used as alternatives to these MBP peptides in these compositions.
                                                                           AAW43951;
                                                                                                        AAW43951 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+T-cell mediated autoimmune disease which results in demyelination of the central nervous system, resulting in paralysis and other neurological abnormalities. EAE is a commonly used animal model for human multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR95334-R95374 represent peptides derived from myelin basic protein (MBP). Immunisation with MBP can be used to induce experimental alleencephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-MAR-1995;
25-OCT-1994;
25-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Myelin basic derived peptide(s) and analogs - used in of Multiple Sclerosis, psoriasis, Graves Disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rothbard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Devaux B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CNS; animal model; human; multiple sclerosis; MS; mammal; benign relapsing-remitting MS; chronic progressive MS; myelin autoantigg diabetes; Graves disease; myasthenia gravis; Good Pasture's syndipsoriasis; thyroiditis; rheumatoid arthritis; proteolipid proteir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     myelin
                                                                                                                                                                                                                   1 ISRFAWG 7
                                                                                                                                                 ø
                                                                                                                                                                                                  lsrfswg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oligodendrocyte protein;
                                                                                                                                                                                                                                                                                                                                                                19 AA;
                                                                                                                                                                                                                                                                        Conservative
basic protein peptide MBP-3.1 (111-129).
                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  95US-0404228.
94US-0328224.
95ZA-0009033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95WO-US13682
                                                                                                                                                                                                                                                                                       71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gefter N
Shi J,
                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                     Score 35; DB Pred. No. 4.8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          M, Hsu D,
, Smilek D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Paliard
                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                    Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein; MAG;
                                                                                                                                                                                                                                                               Gaps
```

22222222

Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis; autoimmune response; MBP; myelin basic protein; demyelinating.

(IMMU-) IMMULOGIC PHARM CORF

Ş

```
RESULT
AAR95394
В
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity /1...
S; Conservative
                    15-MAR-1995;
25-OCT-1994;
25-OCT-1995;
                                                                                                                                                                                        CD4+; T-cell; autoimmune disease; demyelination; central nervous system; CNS; animal model; human; multiple sclerosis; MS; mammal; benign MS; MOG; relapsing remitting MS; chronic progressive MS; myelin autoantigen; PLP; diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome;
                                                                                                                                                                                                                                  Myelin basic protein; MBP; experi
CD4+; T-cell; autoimmune disease;
                                                                      25-OCT-1995;
                                                                                               02-MAY-1996
                                                                                                                      WO9612737-A2
                                                                                                                                                                      myelin oligodendrocyte
                                                                                                                                                                                   psoriasis; thyroiditis;
                                                                                                                                                                                                                                                                      Residues 101-120 of myelin basic protein.
                                                                                                                                                                                                                                                                                                                                                  AAR95394 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a novel peptide of human myelin basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte glycoprotein) and MBP can be used to treat multiple sclerosis in a mammal by down-regulating an autoimmune response in the mammal. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                can also be used to diagnose and treat other diseases in humans, or to prepare antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human myelin oligodendrocyte glyco-protein peptide - useful multiple sclerosis in mammal by down-regulating auto-immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Devaux B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                             10
                                                                                                                                                                                                                                                                                                                                                                                                                  1 lsrfswg 7
                                                                                                                                                                                                                                                                                                                                                                                                                                         1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19
                                                                                                                                                                                                                                                                                                (first entry)
                    94US-0328224.
95ZA-0009033.
                                             95US-0404228
                                                                    95WO-US13682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96US-0623406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US06072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              diagnose and treat other demyelinating autor to prepare antibodies for the detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108pp; English.
                                                                                                                                                                      protein;
                                                                                                                                                                              rheumatoid arthritis; proteolipid protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rothbard J,
                                                                                                                                                                                                                                        experimental allergic encephalomyelitis; EAE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 35; |
Pred. No. 4
2; Mismatch
                                                                                                                                                                                                                                                                                                                                                   20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Smilek D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 18; Length 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wallner
                                                                              ė,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          response
                                                                                                                                                                therapy
```

```
RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mice. EAE is a CD4+ T-cell mediated autoimmune disease which results in demyelination of the central nervous system, resulting in paralysis and other neurological abnormalities. EAE is a commonly used animal model for human multiple sclerosis (MS). These sequences can be used in compositions for treating MS in a manmal. The composition acts to down regulate the autoimmune response, and may be administered in an amount sufficient to prevent the onset of symptoms of MS. The compositions may also be used to treat advanced stage MS, especially relapsing-remitting MS, Chronic progressive MS or benign MS. These peptides may also be used in the treatment of other diseases involving myelin autoantigens, including diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome, psoriasis, thyroiditis, and rheumatoid arthritis. Peptides
15-MAR-1995;
25-OCT-1994;
25-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                               Myelin basic protein; MBP; experimental allergic encephalomyelitis; EAE; CD4+; T-cell; autoimmune disease; demyelination; central nervous system; CNS; animal model; human; multiple records; MS; mammal; benign MS; MOG; relapsing-remitting MS; chronic progressive MS; myelin autoantigen; PLP; diabetes; Graves disease; myasthenia gravis; Good Pasture's syndrome; psoriasis; thyroiditis; rheumatoid arthritis; proteolipid protein; MAG;
                                                                                                                                                                     02-MAY-1996
                                                                                                                                                                                                                             W09612737-A2
                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                       myelin oligodendrocyte protein; myelin associated glycoprotein; therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MBP-3 (111-130)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR95344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR95344 standard; peptide; 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein (MOG), proteol:
glycoprotein (MAG) can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 derived from other myelin autoantigens, such as myelin oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      myelin basic protein (MBP). Immunisation with MBP can be use experimental allergic encephalomyelitis (EAE) in susceptible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 3; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Myelin basic derived peptide(s) and analogs - used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Devaux B, Rothbard J,
                                                                                                                25-OCT-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11 lsrfswg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Franzen H,
Samson M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
95US-0404228.
94US-0328224.
95ZA-0009033.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         proteolipid protein
                                                                                                             95WO-US13682.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and AAR95387-R95397 represent peptides derived from tein (MBP). Immunisation with MBP can be used to induce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gefter M,
Shi J, S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         $
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smilek D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Graves
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PLP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disease, etc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            and myelin associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paliard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17; Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        strains of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
```

```
QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW43950
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               autoimmune response, and may be administered in an amount sufficient to prevent the onset of symptoms of MS. The compositions may also be used to treat advanced stage MS, especially relapsing-remitting MS, chronic progressive MS or benign MS. These peptides may also be used in the treatment of other diseases involving myelin autoantigens, including diabetes, Graves disease, myasthenia gravis, Good Pasture's syndrome, psorlasis, thyroiditis, and rheumatoid arthritis. Peptides derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MBP). Immunisation with MBP can be used to induce experimental allergic encephalomyelitis (EAE) in susceptible strains of mice. EAE is a CD4+ r-cell mediated autoimmune disease which results in demyelination of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR95334-R95374 represent peptides derive (MBP). Immunisation with MBP can be used
                                                                                                                                                                                                                                                                                     Human; myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis; autoimmune response; MBP; myelin basic protein; demyelinating.
                                                                                                                                                                                                                                                                                                                                                                                                        AAW43950;
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW43950 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 other myelin autoantigens, such as myelin oligodendrocyte protein (MOG), proteolipid protein (PLP), and myelin associated glycoprotein (MAG) can be used as alternatives to these MBP peptides in these compositions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              central nervous system, resulting in paralysis and other neurological abnormalities. EAE is a commonly used animal model for human multiple sclerosis (MS). These sequences can be used in compositions for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Myelin basic derived peptide(s) and analogs - used in the treatment of Multiple Sclerosis, psoriasis, Graves Disease, etc.
                            WPI; 1997-489564/45
                                                                                                                           28-MAR-1996;
                                                                                                                                                        01-MAY-1996;
                                                                                                                                                                                                                          WO9735879-A1
                                                                                                                                                                                                                                                                                                                                     Human myelin basic protein peptide MBP-3 (111-130).
                                                                                                                                                                                                                                                                                                                                                                        22-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rothbard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (IMMU-) IMMULOGIC PHARM CORP
                                                            Devaux B,
                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  treating MS in a mammal.
                                                                                         (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 lsrfswg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ISRFAWG 7 :|||:||
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
5; Conserv
                                                           Garman RD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Franzen H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Samson M,
                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                           96US-0623406
                                                                                                                                                          96WO-US06072
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      71.4%;
71.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gefter M,
Shi J, S
                                                           Rothbard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The composition acts to down regulate the
                                                                                                                                                                                                                                                                                                                                                                                                                                       20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M, Hsu D,
Smilek D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               derived
                                                           Smilek D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Paliard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                            Wallner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
```

Human myelin oligodendrocyte glyco-protein peptide - useful to treat

```
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Watches 5; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW44066
Query Match 71.4
Best Local Similarity 71.4
Matches 5; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LI
                                                                                                                                         can also be used to diagnose and treat other diseases in humans, or to prepare antibodies
                                                                                                                                                                      basic protein (MBP). The pept glycoprotein) and MBP can be mammal by down-regulating an
                                                                                                                                                                                    The present sequence represents a novel peptide of human myelin basic protein (MBP). The peptide of human MOG (myelin oligodend glycoprotein) and MBP can be used to treat multiple sclerosis in
                                                                                                                                                                                                                                                                                   Human myelin oligodendrocyte glyco-protein peptide - useful multiple sclerosis in mammal by down-regulating auto-immune
                                                                                                                         diagnosis
                                                                                                                                                                                                                                                             Disclosure;
                                                                                                                                                                                                                                                                                                                                           WPI; 1997-489564/45
                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                              28-MAR-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09735879-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human myelin basic protein peptide MBP-K (101-120).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44066 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                           (IMMU-) IMMULOGIC PHARM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              02-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW44066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a novel peptide of human myelin basic protein (MBP). The peptide of human MOG (myelin oligodendrocyte glycoprotein) and MBP can be used to treat multiple sclerosis in a mammal by down-regulating an autoimmune response in the mammal. They can also be used to diagnose and treat other demyelinating autoimmune diseases in humans, or to prepare antibodies for the detection or diagnosis of autoimmune diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              multiple sclerosis in mammal by down-regulating auto-immune response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 101; Page 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 :|||:||
                                                                                                                                                                                                                                                                                                                                                                              8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       myelin oligodendrocyte glycoprotein; MOG; multiple sclerosis; mune response; MBP; myelin basic protein; demyelinating.
                                                                                                                      of autoimmune
                                                                                        20
                                                                                                                                                                                                                                                                                                                                                                              Garman RD,
                                                                                                                                                                                                                                                         Page 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                        ξ
                                                                                                                                                                                                                                                                                                                                                                                                                                            96US-0623406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96WO-US06072
                   71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 108pp;
                                                                                                                                                                                                                                                      108pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
71.48;
                                                                                                                                     to prepare antibodies for the detection or
                                                                                                                                                                                                                                                                                                                                                                          Rothbard J,
   Score 35; DB Pred. No. 5; 2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    English
                                                                                                                                                                 used to treat multiple sclerosis in a autoimmune response in the mammal. They
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                          Smilek D, Wallner B;
                    DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DΒ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
                                                                                                                                                   demyelinating autoimmune
   0;
                                                                                                                                                                                                     (myelin oligodendrocyte
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                  Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ļength
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20;
 0;
                                                                                                                                                                                                                                                                                                     to treat
                                                                                                                                                                                                                                                                                     response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
```

Ş

826666666666

RESULT 15 AAB12619

g. Š

l lsrfswg 1 ISRFAWG Matches

l Similarity 5; Conserv

Conservative

2

Mismatches

0;

Indels

0

Gaps

0

of

```
PA XXX PA XXX PA XXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                          PR
PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PD XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΧX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              XSXXXX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 1
AAW73618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             XX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
  Query Match
Best Local
                                                                          This sequence represents a fragment of the human myelin basic protein (MBP). The peptides are immunodominant regions of MBP, and are used as the immunosuppressant agents of the invention. The peptides act on the response to MBP (or tissues containing it), specifically for treatment of T cells or actively suppress these cells by inhibiting their proliferation, possibly by inducing suppressor T cells. The peptides may also be used to detect specific T cells. The MBP fragments do not induce patient developing certain malignancies), will not down regulate normal immune responses to pathogenic micro-organisms and are less toxic than drugs currently used for the treatment of MS, such as azathioprine (Imuran), and cyclosporin A.
                                                                                                                                                                                                                                                                                                                                                                                                                               28-FEB-1992;
09-APR-1992;
06-JUN-1995;
                                                     Sequence
                                                                                                                                                                                                                                                                  Example 1; Column 13-14; 32pp;
                                                                                                                                                                                                                                                                                                           New peptides from immunodominant protein - useful as immunosuppres
                                                                                                                                                                                                                                                                                                                                                                          Al-Sabbagh A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Myelin basic protein; MBP; human; immunodominant region; inhibitor; immunosuppressant agent; multiple sclerosis; T cell proliferation;
                                                                                                                                                                                                                                                                                               sclerosis
                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-119958/10.
                                                                                                                                                                                                                                                                                                                                                                                                      (AUTO-) AUTOIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     09-APR-1993;
30-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US5858980-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    suppressor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAW73618;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW73618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11 lsrfswg 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               щ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    standard;
                                                                                                                                                                                                                                                                                                        useful as immunosuppressants
                                                     20
                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                             92US-0843752.
92US-0865318.
95US-0468540.
                                                                                                                                                                                                                                                                                                                                                                            Hafler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    930S-0046354
900S-0502559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0468540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
 71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                        DA,
                                                                                                                                                                                                                                                                                                                                                                         Miller A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     residues 113-132
Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20
                                                                                                                                                                                                                                                                   English
                                                                                                                                                                                                                                                                                                       regions of human myel
ssants for treatment o
                                                                                                                                                                                                                                                                                                                                                                         Weiner
            ВB
            20;
                                                                                                                                                                                                                                                                                                                                                                         HL
            Length 20;
                                                                                                                                                                                                                                                                                                        o
f
                                                                                                                                                                                                                                                                                                                     in
                                                                                                                                                                                                                                                                                                       n basic
multiple
                                                                                                                                                                                                                                                                                                                   basi
```

```
Query Match
Best Local Similarity
"---hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-APR-1993;
30-MAR-1990;
28-FEB-1992;
09-APR-1992;
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               neuroprotective and immunosuppressive activities. The compositions and peptides from the present invention are useful in suppressing multiple sclerosis, which is due to the induction of CD8+ suppressor T-cells. The peptides are also useful in identifying CD4+ T-cells reactive with myelin basic protein (MBP). The peptides are also useful in identifying individuals with T-cells reactive to MBP. Oral administration of MBP suppressed central nervous system (CNS) inflammation in actively induced experimental allergic encephalomyelitis (EAE). There was a decreased inflammation in both the parenchyma and meninges when cells from MBP-fed animals were transferred. This suppression was observed when CNA+ denoted but not CD8+
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New pharmaceutical composition comprising peptide fragments of myelin basic protein, useful in suppressing the symptoms of multiple sclerosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-450923/39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; myelin basic protein; MBP; multiple sclerosis; MS; CNS; immunodominant; chronic inflammatory disease; central nervous system; autoimmune disease; neuroprotective; immunosuppressive; CD8+; CD4+.
                                                                                                                                                                                                                                                                                                                                                    present invention
                                                                                                                                                                                                                                                                                                                                                                           when CD4+ depleted, but not CD8+. The present sequence represents human MBP peptide fragment, which is used in an example from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Column 14; 26pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hafler DA, Weiner HL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (AUTO-) AUTOIMMUNE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US6077509-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human myelin basic protein peptide 113-132.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAB12619 standard; peptide; 20 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a pharmaceutical formulation comprising peptide having a 30-amino acid sequence (AAB12612) (I) or a segment of (I), provided that the segment comprises at least the 19-amino acid sequence given in AAB12613. The pharmaceutical formulation has
1 ISRFAWG 7
:|||:||.
1 lsrfswg 7
                                                                                                                                                                                                                                                                                     20
                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93US-0046354.
90US-0502559.
92US-0843752.
92US-0865318.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           95US-0469648.
                                                                                                                                                    71.48;
71.48;
                                                                                                                   Score 35; DB 21; Length 20; Pred. No. 5; 2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                               The present sequence represents a
                                                                                                                      ö
                                                                                                                Gaps
```

earch completed: October 18, 2001, 16:51:16 ob time: 41 sec

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   '.mum DB seq length: 0
Lmum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/
2: /cgn2_6/ptodata/2/
3: /cgn2_6/ptodata/2/
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-646-579-2
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              197339 seqs, 20590346 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           October 18, 2001, 16:51:41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/6B_COMB.pep:*
/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
 US-08-781-122-2
US-09-137-759-2
US-08-735-253-7
US-08-735-253-7
US-08-735-253-12
US-08-888-497-40
PCT-US94-07926-40
US-08-888-497-32
PCT-US94-07926-32
US-08-633-768A-1
US-08-933-768A-1
US-08-933-768A-1
US-08-33-768A-1
US-08-33-768A-1
US-08-33-768A-1
US-09-234-613-22
US-08-451-715A-8
                                                                                                                                                                                                                                                                                                                                                                    US-08-159-339A-1078
US-08-735-253-1
US-08-468-540B-11
US-08-297-395-23
                                                                                                                                                                                                                                                                                                       US-08-227-372-1
US-08-327-357A-1
US-08-470-397-1
                                                                                                                                                                                                                                                                          US-09-007-520-1
US-08-462-351-3
                                                                                                                                                                                                                                                           US-09-055-263-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search time 18.9 Seconds (without alignments) 9.805 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   197339
                                                                                                                                                                                                                          Patent No.
Patent No.
                                                                                                                                                                                                                               Sequence 1, Appli
Sequence 3, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
                                                                                                                                           Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                     Patent No.
                                                                             Sequence
Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                       Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                   Sequence
Sequence
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                               Description
                                  Sequence
                                               Sequence
                                                                Sequence
                                                                                                                                                                                         Sequence
                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                         2, Appli
2, Appli
2, Appli
6, Appli
6, Appli
12, Appli
12, Appl
                                                                                                                                                                                                                                                                   1, Appli
1, Appli
1, Appli
1, Appli
1, Appli
3, Appli
                                                                                                                                                                                                                                                                                                                                                   11, Appl
23, Appl
5194425
                                                                                                                                                                                                                                                                                                                                                                                                 1078, Ap
1, Appli
                                             Appli
Appli
Appl
```

45	44	43	42	41	40	9	38	37	36	i Li	4	(L)	32	31	30	29	28
30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	30	. 30	32
61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	61.2	65.3
636	636	623	623	623	578	578	578	461	321	321	321	263	263	263	111	111	1621
N	_	ω	N	۲	w	N	_	5	G	w	۳	S	w	_	4	س	4
US-09-073-594-5	US-08-653-740-5	US-09-275-925-7	US-09-073-594-7	US-08-653-740-7	US-09-275-925-3	US-09-073-594-3	US-08-653-740-3	PCT-US93-12464-2	PCT-US94-14030A-26	US-08-333-576C-26	US-08-362-670B-26	PCT-US94-14030A-32	US-08-333-576C-32	US-08-362-670B-32	US-08-469-617-36	US-08-466-886-36	US-08-972-927-3
Sequence 5, Appli	Sequence 5. Appli	Sequence 7. Appli	Sequence 7. Appli	Sequence 7. Appli	Sequence 3. Appli	Sequence 3. Appli	Sequence 3. Appli			Sequence 26, Appl						36.	Sequence 3. Appli

ALIGNMENTS

ptides and Crew Eighth Flo	INFORMATION FOR SEQ ID NO: 1078: SEQUENCE CHARACTERISTICS: LENGTH: 9 amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide	ATE: 07-AUG-1992 FION NUMBER: US 08/027,74 ATE: 05-AWR-1993 FION NUMBER: US 08/103,39 FION NUMBER: US 08/103,39 FION NUMBER: US 08/103,39 ATE: 06-AUG-1993 GENT INFORMATION: VITON NUMBER: 32,762 VITON NUMBER: 32,762 VITON NUMBER: 018623- VICATION INFORMATION: US: (415) 576-0300 (415) 576-0300	San Francisco CA USA 4111-3834 4111-3834 FIREADABLE FORM: TYPE: Diskette TYPE: Diskette E: FastcEQ for Windows Ve PPLICATION DATA: IOATION: 424 LICATION DATA: ICATION DAT	Patent No. 6037135 GENERAL INFORMATION: APPLICANT: Kubo, Ralph T. APPLICANT: Sette, Alessandro APPLICANT: Celis, Esteban TITLE OF INVENTION: Uses UMBER OF SEQUENCES: 1254 CORRESSEE: Townsend and Townsend and C STREET: Two Embarcadero Center, Eighth
----------------------------	--	---	--	---

```
S-08-735-253-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    JS-08-159-339A-1078
                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide;-08-735-253-1
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                      Matches
                                                                                     Sequence 11, Application US/08468540B
                                                                                                                  -08-468-540B-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (3120 616-54 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET: 10.
TTTY: Chicago
TTTY: Tilinoi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: MIC3302P0010US ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTORNEY/AGENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-POS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PPLICATION NUMBER: US/08/735,253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISRFAWG 7
                                                                                                                                                                            LSRFSWG
                                                                                                                                                                                                        ISRFAWG
                                                                         INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60601
                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No. 5942491thrup,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08735253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     180 N. Stetson
                                                                                                                                                                                                                                                                                                                                                                                 12 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U.S.A.
                             Miller, Ariel
                                                        Weiner, Howard
                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                              (3120 616-5460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Root-Bernstein, Robert S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dressler, Goldsmith, Milnamow & Katz, Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                            David
                                                                                                                                                                                                                                                                                                                                                                                                                                            616-5400
                                                                                                                                                                                                                                                 71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arthritis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Methods and Compositions for Treating
SUPPRESSION OF T-CELL PROLIFERATION
                                                                                                                                                                                                                                                 Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                                                                                   DB 2;
1.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5e+05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 9;
                                                                                                                                                                                                                                                               Length 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VΩ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
"~* hes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-468-540B-11
SEQ ID NO 23
LENGTH: 20
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                3-08-25,
Sequence 23, App.
+ No. 603994
                                                                                                                                                                                            CURRENT
EARLIER
                                                                                                                                                                                                                                         APPLICANT: DAVId A. HAFIET
TITLE OF INVENTION: PEPTIDES I
TITLE OF INVENTION: EPITOPES (
FILE REFERENCE: 1010/05723US3
                                                                                                                                                                                                                                                                                                                         ENERAL INFORMATION:
                                              SOFTWARE:
                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/297,395A
                                                                                                                                                                                                                                                                                         APPLICANT: Howard
                                                                                           SARLIER APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-527-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Jacobs, Seth H
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      .1 LSRFSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ISRFAWG
                                                                 OF SEQ ID
                                                                                                          FILING DATE: 1988-06-24
                                                                                                                           APPLICATION NUMBER: PCT/US88/02139
                                                                                                                                                         APPLICATION NUMBER: 07/502,559
                                                                                                                                                                           APPLICATION NUMBER: 08/059,189 FILING DATE: 1993-05-06
                                                                                                                                                                                                         FILING DATE: 1994-08-11
                                                                                                                                          FILING DATE: 1990-03-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10022
                                              FastSEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                    Application US/08297395A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Darby & Darby P.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Third Avenue
                                              for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 5858980e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             single
                                                                                                                                                                                                                                                                     PEPTIDES DERIVED FROM IMMUNODOMINANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USING PEPTIDE FRAGMENTS OF MYELIN BASIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US/08/468,540B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        32,140
                                                                                           07/065,734
                                                                                                                                                                                                                                                        OF MYELIN BASIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
```

0;

```
5194425-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Thes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; ORGANISM: Homo sapiens
US-08-297-395-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NO:4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No. 5194425

APPLICANT: SHARMA , SOMESH D.; LERCH, L. BERNARD; CLARK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMELIORATING AUTOIMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BRIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -08-227-372-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /equence 1, Apr. 2763585
                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/136,216
FILING DATE: 13-OCT-1993
                                                 FILING DATE: 13-OCT-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nag, Bishwajit
TITLE OF INVENTION: PURIF
TITLE OF INVENTION: MHC-PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   109 LSRFSWG 115
                                                                                                                     CLASSIFICATION:
                                                                                                                                   APPLICATION NUMBER: FILING DATE: 14-APF
                                                                                                                                                                                                                                                                                                                      STREET: Steuart Str
CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 23-JUN-1988
                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                          DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||:||
                                                                                                                                                                                                                                                                         94105-1493
                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08227372
                                                                                                                                                                                                                                                                                                                                      E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                   14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21-JUN-1989
NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                    PURIFICATION AND CHARACTERIZATION OF MHC-PEPTIDE COMPLEXES USEFUL IN AMELIORATING AUTOIMMUNITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     210,594
                                                                                                                                                   US/08/227,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      us/07/367,751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pred. No. 22;
2; Mismatches
14058-32-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. 2.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION: 1..170
; OTHER INFORMATION:
US-08-227-372-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-327-357A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1, Application US/08327357A Patent No. 5817629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                         NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 543-50 INFORMATION FOR SEQ ID NO:
                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-OCT-
                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
                                                                                                                                        ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111 LSRFSWG 117
                                                                                                                                                                NAME: Ihnen, Jeffrey L. REGISTRATION NUMBER: 28,957
                            STRANDEDNESS:
                                                                                                                           TELEPHONE:
                                                                                                                                                         REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                              APPLICATION NUMBER: US 0 FILING DATE: 27-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Protein LOCATION: 1..170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        20005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington
                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201 New York Avenue,
                                                                                                            202-962-8300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WARREN, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 unknown
                                                                                                                                                                                                                                                                                                                                                                     Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESS:
                                                                                                                                                                                                                   UMBER: CA 2,053,799-0
22-0CT-1991
peptide
                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein
                                                                                                                                                                                                                                                                                                                             21-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ingri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC
                                                                                                                                                                                                                                                                                                                                          US/08/327,357A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Myelin basic protein"
                                                                                                                                                                                                                                                                              US 07/798,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Baetjer,
                                                                                                                                                      27052-115469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Howard & Civiletti
, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MUTIPLE SCLEROSIS PATIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB
22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 170,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BASIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
```

```
US-08-470-397-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-327-357A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Loc
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              equence 1, Application US/08470397 tent No. 6007820
                                                                                                                                                                                                                                                                          NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ENERAL INFORMATION:
APPLICANT: Nag, B
                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14 TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Rel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: human myelin basic protein
                                                                                                                                                                            HOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Nag, Bishwajit
NITLE OF INVENTION: Purification and Characterization of
NITLE OF INVENTION: MHC-Peptide Complexes Useful in Ameliorating Autoimmunity
                                                                                                                                                             YPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            111 LSRFSWG 117
                                                                             OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US 0: FILING DATE: 13-OCT-1993
 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 5; Conserv
                                                                                                                           NAME/KEY: Modified-site
                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER:
                                 LOCATION:
                                                NAME/KEY:
                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  94105-1492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                San Francisco
California
                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                   /AGENT · INFORMATION :
                                                                                                                                                                                                                                                                                                                                                                  Bastian, Kevin L
                                                                                                                                                                                                                                          170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: Townsend and Townsend and Crew
One Market Plaza, Steuart Street
                                                                                                                                                                                                                                                                                         (415)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                         linear
                                              Modified-site
                                                                                                                                                             protein
NO
                                                                                                                                                                                                                                                                                                           (415)
                                                                                                                                                                                                                                                                                                                                                                                                      UMBER: US 08/227,372
14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-1995
                                                                                                                                                                                                                                                                                                        543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US 08/136,216
/product- "OTHER"
/note- "Xaa - Ala
                                                                             /product= "OTHER"
/note= "Xaa = N-ac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/470,397
                                                                                                                                                                                                                                                                                                                                                     34,774
                                                                                                                                                                                                                                                                                                                                        14058-32-1-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2;
"Xaa - Ala or absent"
                                                                             "Xaa = N-acetyl-alanine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 35; DB Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steuart Street Tower, 20th
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DВ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
```

밁 Ω

111 LSRFSWG 117

1 ISRFAWG 7

Conservative

0;

Indels

0; Gaps

ç

```
Query Match
Best Local Similarity
""+"hes 5; Conserv
                                                                      US-08-470-397-1
                                                                                                                                                                                                                                                                                                      FEATURE:
                                                                                                                     FEATURE:
                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                               FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                  NAME/KEY:
                                                                                            NAME/KEY:
                                                                                                                               OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                  OTHER INFORMATION:
                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                             LOCATION:
                                                                                                                                                                                                                                                                                         NAME/KEY:
                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                        LOCATION:
                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INFORMATION: INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                             Protein
1..170
                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                   Modified-site 141
                                                                                                                                                                                                                                                                              08
                                                                                                                                                                                                                                                                                        Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                     Modified-site 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Modified-site
                      71.48;
71.48;
                                                                              /note= "Myelin basic protein"
                                                                                                                                                                                         /product- "OTHER"
/note- "Xaa - Leu
                                                                                                                                                                                                                                                  /product= "OTHER"
/note= "Xaa = Pro
                                                                                                                                                                                                                                                                                                              /product= "OTHER"
/note= "Xaa = Gln
                                                                                                                               /product= "OTHER"
/note= "Xaa = His
                                                                                                                                                                                                                                                                                                                                                                         /product= "OTHER"
/note= "Xaa = Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "OTHER"
/note= "Xaa = Thr or Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "OTHER"
/note= "Xaa = Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product= "OTHER"
/note= "Xaa = Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "OTHER"
/note= "Xaa = Ser or Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "OTHER"
/note= "Xaa = Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "OTHER"
/note= "Xaa = Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "OTHER"
/note= "Xaa = Arg
                     Pred. No.
                                                                                                                                                                                         "Xaa = Leu or Phe"
                                                                                                                                                                                                                                                                                                                                                                           "Xaa - Ala or Ser"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Xaa - Arg or His"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Xaa = Gly or Ser"
                                                                                                                                His or Val*
                                                                                                                                                                                                                                                    Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ser or Thr'
                     DB
22;
                                                                                                                                                                                                                                                    or Thr'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or Gly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ç
                                                                                                                                                                                                                                                                                                              or absent"
                                 Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ile"
                                 Length 170;
```

```
us-09-007-520-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 9
US-09-007-520-1
                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 5; Conser
                                Sequence 3, Application US/08462351
Patent No. 6106840
                                                               08-462-351-3
                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 20
NFORMATION FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            equence 1, Application US/09007520 stent No. 6103696
                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                            111 LSRFSWG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                 NIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                               EQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORRESPONDENCE ADDRESS:
                                                                                                                                               1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                    ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/09/007,520
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                              POLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ER OF SEQUENCES:
                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20005
                                                                                                                                                                                                                                                                                                                                                                                               amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington
                                                                                                                                                                                                                                                                                 human myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                            170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1201 New York Avenue,
Sharma, Somesh D.
                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATZ, Ingrid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WARREN, Kenneth G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Venable,
                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jeffrey L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-OCT-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PEPTIDES TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CA 2,053,799-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Baetjer, Howard & Civiletti
rk Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08/327,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28,957
                                                                                                                                                                                                     Score 35; DB
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27052-115469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THE ADMINISTRATION MUTIPLE SCLEROSIS

 Length 170;

                                                                                                                                                                                   0;
                                                                                                                                                                                   Gaps
                                                                                                                                                                                   0,
```

EATURE:

NAME/KEY:

Modified-site

OTHER INFORMATION: OTHER INFORMATION:

/product= "OTHER"
/note= "Xaa = Ser or Gly"

NAME/KEY: LOCATION:

Modified-site

```
TELEFAX: (415)
NFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                              OLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION:
                                                                                                            LOCATION: 3
OTHER INFORMATION:
 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                              OTHER INFORMATION:
                                                                                OTHER INFORMATION:
                                                                                                                                                 NAME/KEY:
                                   LOCATION:
                                                  NAME/KEY:
                                                                                                  OTHER INFORMATION:
                                                                                                                                                                                                              LOCATION:
                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                               LOCATION:
                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                               COPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                            ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               California
                                                                                                                                                                                                                                                                                                                                                                                          170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Two Embarcadero Center,
                                              Modified-site
                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PatentIn Release #1.0,
                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Townsend and Townsend and Crew LLP combarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                              (415)
                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JMBER: US 07/210,594
23-JUN-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       23-APR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Annette
                                                                                                                                                                                                                                                                                                                                                                                                                                           576-0300
                                                                                                                                                                                                                                                                                                                                                                                                                                                              576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Autoimmunity
                                                                                                                                                                            /product= "OTHER"
/note= "Xaa = N-a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MHC Conjugates Useful in Ameliorating
/product= "OTHER"
/note=:"Xaa = Arg
                                                                                                                                                                                                                                                         /note= "myelin basic protein (MBP)"
                                                                                or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         us 07/869,293
                                                                                          /product= "OTHER"
/note= "Ala at position 3 may be present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US 07/690,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/576,084
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/462,351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       42,058
                                                                                                                                                                                                                                                                                                                                                                                                                            ω
··
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        014058-0002420S
"Xaa = Arg or His"
                                                                                                                                                                            "Xaa = N-acetyl-alanine"
```

```
Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                    OTHER INFORMATION:
OTHER INFORMATION:
US-08-462-351-3
111
                                                                                                                                                                                        EATURE:
                                                                                                                                                             NAME/KEY:
LOCATION:
                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: OTHER INFORMATION:
              1 ISRFAWG 7
                                                                                                                                                                                                                 OTHER INFORMATION:
                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                  LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VAME/KEY:
LSRFSWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
INFORMATION:
                                                    Conservative
                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                                                                                                                                                 Modified-site
107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Modified-site
                                                                                                                                                                                                                                           Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                               Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Modified-site
                                                                                                                                                                          Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Modified-site
                                                               71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product= "OTHER"
/note= "Gln at position 76 may
present or absent"
                                                                                                                                /product- "OTHER"
/note- "Xaa - His
                                                                                                                                                                                                  /product= "OTHER"
/note= "Xaa = Leu
                                                                                                                                                                                                                                                                   /product= "OTHER"
/note= "Xaa = Lys
                                                                                                                                                                                                                                                                                                                                      /product= "OTHER"
/note= "Xaa = Arq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "OTHER"
/note= "Xaa = Gly or Ser"
                                                                                                                                                                                                                                                                                                                                                                                                       /product= "OTHER"
/note= "Xaa = Pro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product= "OTHER"
/note= "Xaa = Thr or Ala"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "OTHER"
/note= "Xaa = Ala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product= "OTHER"
/note= "Xaa = Ser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product= "OTHER"
/note= "Xaa = Leu or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= "OTHER"
/note= "Xaa = Ser or Thr"
                                                               Score 35;
Pred. No.
                                                                                                                                                                                                "Xaa = Leu or Phe"
                                                                                                                                 "Xaa - His or Val"
                                                                                                                                                                                                                                                                    "Xaa = Lys or Arg"
                                                                                                                                                                                                                                                                                                                                      "Xaa - Arg or Met"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Xaa = Ala or Ser"
                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Pro or Thr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ser or Gly*
                                                                            Ψ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ile"
                                                 0; Indels
                                                                         Length 170;
                                                 0;
                                              Gaps
                                               0;
```

RESULT 11 US-09-055-263-1

Sequence 1, Application US/09055263

```
RESULT 12
5194425-3
;Patent No. 5194425
; APPLICANT: SHARMA
                                                                                                                                                                                                                          8
                                                                                                                                                                                                                                                           ş
                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                             US-09-055-263-1
                                                                     TITLE OF INVENTION: MHC-MEDIATED TOXIC CONJUGATES USEFUL IN AMELIORATING AUTOIMMUNITY
                                                                                                     BRIAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 202-962-8300
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
NUMBER OF SEQUENCES: 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/367,751
FILING DATE: 21-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: human myelin basic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION:
FILING DATE: 22-CL
ATTORNEY/ACENT INFORMATION:
ATTORNEY Innen, Jeffrey L.
Thnen, Jeffrey L.
28,957
                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 27 TELECOMMUNICATION INFORMATION: TELEPHONE: 202-962-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: CA 2,053,799-0
FILING DATE: 22-OCT-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 20005

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                        111 LSRFSWG 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                           1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 21-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 27-NOV-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               E: Venable, Baetjer, Howard & Civiletti
1201 New York Avenue, N.W., Suite 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATZ,
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WARREN, Kenneth G. CATZ, Ingrid
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                             peptide
                                                                                                               , SOMESH D.; LERCH, L. BERNARD; CLARK,
                                                                                                                                                                                                                                                                                                        71.48;
71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEPTIDE SPECIFICITY OF ANTI-MYELIN BASIC PROTEIN PROTEIN AND THE ADMINISTRATION OF MYELIN BASIC PROTEIN PEPTIDES TO MUTIPLE SCLEROSIS PATIENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US 07/798,099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/327,357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US/09/055, 263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <u>..</u>
                                                                                                                                                                                                                                                                                                        Score 35;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   27052-115469
                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                         4
                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                        Length 170;
                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                        0
```

0

5194425-3

LENGTH: 170

FILING DATE: 23-JUN-1988

PRIOR APPLICATION DATA:

210,594

```
Query Match
Best Local Similarity
Thes 5; Conserv
                                                                                                                                                                                                                                                                                    RESULT 14
US-08-781-122-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5468481-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
---hes 5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO:3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5468481
                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                          equence 2, Application US/08781122 atent No. 5948764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: SHARMA, SOMESH D.; CLARK, BRIAN R.; LERCH, BERNARD L. TITLE OF INVENTION: MHC CLASS II-PEPTIDE CONJUGATES USEFUL AMELORIATING AUTOIMMUNITY
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ISRFAWG 7
:|||:||
111 LSRFSWG 117
                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 7
CURRENT APPLICATION DATA:
                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/07/869,293
FILING DATE: 14-APR-1992
PRIOR APPLICATION DATA:
                                                                                                                                                       TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                  111 LSRFSWG 117
                                                            COUNTRY:
                                                                                           CITY: Seattle
                                                                                                       STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 170
                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 28-DEWAPPLICATION NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 690,840
FILING DATE: 23-APR-1991
APPLICATION NUMBER: 576,084
FILING DATE: 30-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                            1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 635,840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 210,594
FILING DATE: 23-JUN-1988
                                                 98104-7092
                                                                           Washington
                                                                                                    E: SEED and BERRY LLP
6300 Columbia Center, 701 Fifth Avenue
                                                               USA
                                                                                                                                                                                                             Conlon,
                                                                                                                                                                                                                           Gaur, Amitabh
                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         28-DEC-
                                                                                                                                                                                                 Nicholas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
71.48;
                                                                                                                                                             METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS
UTILIZING PEPTIDE ANALOGUES OF HUMAN MYELIN BASIC PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                      71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998
367,751
                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 35; DI
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                        Pred.
                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 170;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                , 0;
                                                                                                                                                                                                                                                                                                                                                                                                       .
0;
                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
```

Search completed: October 18, 2001, 16:51:42 Job time: 67 sec

```
망
                                               Query Match
Best Local Similarity
5; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
"~+~hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-781-122-2
                                                                                                                                              JS-09-137-759-2
                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/137,759
CURRENT FILING DATE: 1998-08-20
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 171
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09137759 Patent No. 6251396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -09-137-759-2
                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METHODS FOR TREATMENT OF MULTIPLE SCLEROSIS USING TITLE OF INVENTION: PEPTIDE ANALOGS OF HUMAN MYELIN BASIC PROTEIN FILE REFERENCE: 690068.405C1
                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ling, Nicholas C.
APPLICANT: Staehlin, Theophil
APPLICANT: Crowe, Paul D.
                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Conlon, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Gaur, Amitabh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Maki, David J.
REGISTRATION UNUBER: 31,392
REFERENCE/DOCKET NUMBER: 6900
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (206) 682-60 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
:|||:||
112 LSRFSWG 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              :|||:||
112 LSRFSWG 118
                                 1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/0 FILING DATE: 09-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       171 amino acids
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYSTEM: PC-DOS/MS-DOS
PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/781,122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     690068.418C1
                                                                            Score 35; DE
Pred. No. 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 35; DB Pred. No. 22;
                                                              Mismatches
                                                                                          Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                             Indels
                                                             0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
```

ï

```
Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OM protein -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perfect score:
       imum DB seq length: 0
imum DB seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by character greater than or equal to the score of the results and is derived by analysis of the total score distr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein search, using sw model
                                                                                                                                                                                                                                                                                                         Query
Match
                                                                                                                           PIR_68:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 18, 2001, 16:52:11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   219241 seqs, 76174552 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-646-579-2
49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                piri: * · pir2: * · pir3: * · pir4: *
                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                         BG
  MBBOB
MBCZB
MBPGB
MBHUB
MBHUB
MBMSB
D71537
F81692
E86529
F72092
                                                                                          H75300

$77232

I51632

I51634

MNIV16

MNIVA6

MNIVA6

MNIVA7

MNIVA8

A44575

T30305

T30305

A44625

A44625

A44625

A44625

A44625

A44625
                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search time 22.89 Seconds (without alignments)
29.951 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219241.
 probable replicati
chromosomal replic
replication initia
chromosomal replic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
B35119
Query Match
Best Local Similarity
Matches 7; Conserv
```

45	44	43	42	41	40	39	38	37	36	. U	34	ü	32	31	30
ω ω	ω ω	ω	33	33	33	33	ω ω	34	34	4.	34	34	34	34	35
67.3	67.3	67.3	67.3	67.3	67.3	67.3	67.3	69.4	69.4	69.4	69.4	69.4	69:4	69.4	71.4
463	454	449	336	328	254	254	160	611	592	490	488	237	237	138	639
2	2	2	2	N	N	N	N	N	N	N	N	<u>ب</u>	_	N	N
E86464	D84931	в69759	T41118	T15469	F69547	E69533	T22205	C58893	E75032	C81790	G81213	MNIV1A	MNIV1K	A49959	JC4881
														-	
hypothetical prote	chromosomal replic		hypothetical prote	hypothetical prote	nucleotide-binding	nucleotide-binding	hypothetical prote	NADH dehydrogenase	carbon starvation	conserved hypothet	ັ	nonstructural prot	nonstructural prot	phospholipase A2 (polyvinyl-alcohol

ALIGNMENTS

	. 533113
	4-carboxymuconolactone decarboxylase (EC 4.1.1.44) - Acinetobacter calcoaceticus
	C; Date: 27-Jul-1990 #sequence_revision 27-Jul-1990 #text change 08-sen-1997
	R; Hartnett, C.; Neidle, E.L.; Ngai, K.L.; Ornston, L.N.
	cal coacet i cus
	y divergence.
	A, Accession: B35119 A, Accession: B35119
	A;Status: preliminary
	A; Molecule type: DNA
ance to have a	A; Residues: 1-134 <har></har>
sult being printed,	A;Cross-references: GB:M33798; NID:g141771; PID:g141772
	C;Superfamily: 4-carboxymuconolactone decarboxylase C;Keywords: carbon-carbon lyase; carboxy-lyase
Description	atch cal Sim
4-carboxymuconolac	matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
probable 4-carboxy	QY 1 ISRFANGEV 9
NADH-ubiquinone ox	Db 41 ISRFARGEV 49
4-carboxymuconolac probable lactovidi	
hypothetical prote	REGITT 2
poly(A) polymerase	T47115
nonstructural prot	probable 4-carboxymuconolactone decarboxylase / 3-oxoadipate enol-lactone hydrolase (
	C; Species: Streptomyces sp.
nonstructural prot	C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000 C:Arrossion. #47115
	R; Yang, K.; Iwagami, S.; Davies, J.E.
nonstructural prot	submitted to the EMBL Data Library, May 1999
ronligation - Lac	A; Description: A protocatechuate catabolic gene cluster cloned from Streptomyces sp.
radial spoke prote	A: Welerence number: 224354
myelin basic prote	A/Status: preliminary: translated from GR/FMRI/DDBT
gamma-carboxymucon	A; Molecule type: DNA
basic	A; Residues: 1-373 < YAN>
basic	A;Cross-references: EMBL:AF109386; PIDN:AAD40815.1
myelin basic prote	tal source: strain 2065
basic	A:Gene nost
) contr.
probable replicati	

Conservative

91.8%; 77.8%;

Score 45; DB 2; Pred. No. 0.93; 2; Mismatches

0;

0;

Gaps

0;

Length 3/3; Indels

1 ISRFAWGE

```
A; Cross rerequices our pasce as a strain pasce 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A, Cross-references: EMBL:AL079355; PIDN:CAB45571.1; GSPDB:GN00070; SCOEDB:SC4C6.07c A; Experimental source: strain A3(2) C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The genome sequence of the plant pathogen Xylella fastidiosa A;Reference number: A82515; MUID:20365717
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ş
                                                                                                                                                                                                                                                                                                                                            A; Contents: annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE003884; GB:AE003849; NID:g9105127; PIDN:AAF83118.1; GSPDB:GN00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A, Molecule type: DNA
A; Residues: 1-250 <SIM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: for a complete list
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequer
Nature 406, 151-157, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: E82821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NADH-ubiquinone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   吊
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Gene: pcaL; SCOEDB:SC4C6.07c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Reference number: 221565
A;Accession: T35015
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Seeger, S.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, submitted to the EMBL Data Library, June 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable 3-oxoadipate enol-lactone hydrolase / 4-carboxymuconolactone decarboxylase C;Species: Streptomyces coelicolor C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Д
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q
                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: T35015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                olecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cession: E82821:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      atus: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               286 ISRYAWGEI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity nes 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISRFAWGEV
| | | | : | | | | :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISRYAWGEI 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inone oxidoreductase, NQO5 subunit XF0307 [imported] - Xylella fastidiosa
Xylella fastidiosa
                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ø
                                                                                                                          81.6%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of authors see reference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 88
                                                                                                                      Score 40; I
Pred. No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45;
Pred. No.

    Mismatches

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                       DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .93;
                                                                                                                                                       ν
..
                                                                                     1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ,,
                                                                                                                                                       Length 250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        number A59328 below
                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B.G.; Rajandream,
                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      м. А.
C.Species: Synechocystis sp.
A; Variety: PCC 6803
A; Variety: PCC 6803
C; Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C; Accession: S77232
R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Po, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada
                                                                                                                                                                                                                                                                                        RESULT
S77232
                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                hypothetical protein sll1348 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
```

94

::|:||| VTRYAWGE 101

Synechocystis sp.

(strain

PCC

H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas

1 ISRFAWGE

Similarity 5; Conserv

Conservative

77.6%; 62.5%;

Score 38; DE

DB 2;

Length 126;

Mismatches

0,

0;

```
A; Residues: 1-140 Constant A; Cross-references: GB: AE002054; A; Cross-references: strain R1
                                                                                               A; Molecule type: DNA
A; Residues: 1-126 <WHI>
                                                                                                                                                             A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans A;Reference number: A75250; MUID:20036896 A;Accession: H75300
                                                                                                                                                                                                                       M.; Shen, M.; Vamathevan, J.J.; Lam, P.;
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
                                                                                                                                                                                                                                                                                                                             C; Species: Deinococcus radiodurans C; Date: 03-Dec-1999 #sequence_revi:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
---hes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptomyces coelicolor C;Date: 22-Oct.1999 #sequence_revi. C;Date: T29425
A; Map position: 1
                 A; Gene:
                                      C; Genetics
                                                                                                                                                                                                        A; Title:
                                                                                                                                                                                                                                                                                       R;White,
                                                                                                                                                                                                                                                                                                        C; Accession: H75300
                                                                                                                                          A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                               probable lactoylglutathione lyase - Deinococcus radiodurans (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Note:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, July 1998 A; Reference number: Z20619 A; Accession: T29425
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4-carboxymuconolactone decarboxylase homolog - Streptomyces coelicolor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Residues: 1-449 <PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Parkhill,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      361 LTRYAWGEI 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SC3A7.07
                                                                                                                                                                                                                                                                                O.; Eisen, J.A.; Heidelberg, J.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VGRFAWGE 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                         #sequence_revision 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:AL031155; NID:e1313489; PID:e1313496; PIDN:CAA20070.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     81.6%;
                                                                        GB:AE000513; NID:g6460010; PIDN:AAF11756.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 40;
Pred. No.
                                                                                                                                                                                                                                                           .; Hickey, E
McDonald,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
                                                                                                                                                                                                                                                                                                                     #text_change 31-Mar-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,;
                                                                                                                                                                                                                                                           E.K.; Peterson,
, L.; Utterback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                                                                         J.D.; Dodson,
T.; Zalewski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                      PID:9646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                                                                                                                                                                 꼰
```

```
밁
                                                                                                                                                                                                                                                                                                                                                                                                                                    Ş
                                                                                                                                                                                                                                                                             C;Species: influenza A virus
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                            nonstructural protein NS1 - influenza A virus (strain A/duck/Alberta/60/76)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                   A;Molecule type: genomic RNA
A;Residues: 1-230 <BAE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: EMBL:U23456; NID:g755871; PIDN:AAA64708.1; PID:g755872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  poly(A) polymerase - African clawed frog
                                                                                                                                                                                     ; Accession: A04092
                                                                                                                                                                                                ;;Baez, M.; Zazra, J.J.; Elliott,
/Irology 113, 397-402, 1981
/Title: Nucleotide sequence of th
/Reference number: A04092; MUID:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    \; Molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: EMBL:D90907; GB:AB001339; A; Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: nucleic acid sequence not shown; translation not shown A;Holecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: S77232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA Res. 3, 109-136, 1996
                                                                  ;Keywords: alternative
                                                                                                                                  ;Cross-references:
Query Match
Best Local Similarity
                                                               Map position: segment 8 Superfamily: influenza virus no Superfamily: influenza virus no Superfamily: Maywords: alternative splicing
                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                    Accession: A04092
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          51. Cell. Biol. 15, 1422-1430, 1995
Fitle: Cloning and characterization of a Xenopus poly(A) polymerase;
Reference number: I51681; MUID:95166227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Species: Xenopus laevis (African clawed frog)
Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change;
Accession: I51681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;Gebauer, F.; Richter, J.D.
ol. Cell. Biol. 15, 1422-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; Residues :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                       376 LAMFAWGEI 384
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity hes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                    1 ISRFAWGEV 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISRYAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     type: mRNA: 1-394 <GEB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
5; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       I51681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-289 <KAN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                analysis of the genome of the unicellular cyanobacterium
                                                                                                                                    GB:J02105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S74322; MUID:97061201
   73.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.5%;
                                                                                                                                                                                                                 of the influenza
                                                                              nonstructural protein
                                                                                                                        GB:M17071; NID:g324783; PIDN:AAA43509.1; PID:g324785
 Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
                                                                                                                                                                                                                                                 R.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
No.
 DB
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
27;
                                                                                                                                                                                                                 A/duck/Alberta/60/76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NID:g1652618; PIDN:BAA17566.1; to the EMBL Data Library, June
               <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
               Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 289
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0,
                                                                                                                                                                                                               virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                               SN
                                                                                                                                                                                                             RNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synechocystic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PID:d101829
                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                             conser
                                                                                                                                                             밁
                                                                                                                                                                                          Qy
            R;Treanor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            뫄
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
```

```
C;Species: influenza A virus
C;Date: 31-Mar-1991 #sequence_revision
C;Accession: E32663
                                                                                                                                                                                                                                                                                      A;Map position: segment C;Superfamily: influenza C;Keywords: alternative
                                                  nonstructural protein NS1 -
                                                                    MNIVA7
                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: genomic RNA
A; Residues: 1-230 <TRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Treanor, J.J.; Snyder, M.H.
Virology 171, 1-9, 1989
A;Title: The B allele of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: influenza A virus
C:Date: 31-Mar-1991 #sequence_revision
C:Accession: C32663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NSI
C;Keywords: alternative splicing; nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: A32663
C; Accession: A32663
R; Treanor, J.J.; Snyder, M.H.; London, W.T.; Murphy, virology 171, 1-9, 1989
                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: A32662; A; Accession: C32663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT
MNIVA5
                                                                                                                                                                                                                                                                                                                                             A; Gene: NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nonstructural protein NS1 - influenza A virus (strain A/mailard/Alberta/827/88)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: The B allele of the NS gene of avian influenza viruses, A;Reference number: A32662; MUID:89299445
A;Accession: A32663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
                                                                                                                                                                                                   Query Match
Best Local s
Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Residues: 1-230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Species: influenza A virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nonstructural protein NS1 -
                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                    198 IQRFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                198 IQRFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            198 IQRFAWG 204
                                                                                                                                                                                                                   Local Similarity
                                                                                     12
                                                                                                                                                                      1 ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ISRFAWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6; Conservative
                                                                                                                                                                                                                                                                                                  influenza virus nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Snyder, M.H.; London, W.T.; Murphy, B.R
9, 1989
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <TRE>
                                                                                                                                                                                                                                                                                       splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RNA
                                                                                                                                                                                                                   73.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73.5%;
                                                  influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  influenza A virus (strain A/mallard/Alberta/88/76)
                                                                                                                                                                                                                                                                                                                                                                                                                                       NS gene of avian influenza viruses, but not the A allele
                                                                                                                                                                                                   Score 36; DB
Pred. No. 24;
0; Mismatches
                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0
                                                                                                                                                                                                                                                                                       nonstructural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                             A virus (strain A/pintail/Alberta/121/79)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
            31-Mar-1991 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-Mar-1991
                                                                                                                                                                                                                                   DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                   ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         #text_change
                                                                                                                                                                                                                                   Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B.R.
                                                                                                                                                                                                                                                                                                     SN
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-Apr-1994
                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  but not the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                  0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
```

Virology 171,

Snyder, M.H.; 9, 1989

London,

W.T.; Murphy, B.R

```
A;Cross-references: GB:S39287
A;Note: the authors translated the codon CTG for residue 141 as Gly, CTG: A;Note: sequence extracted from NCBI backbone (NCBIN:108102) and modified C;Superfamily: influenza virus nonstructural protein NS1
                                                                                                                                                                                                                                           R;Perdue, M.L.
Virus Res. 23, 223-240, 1992
Virus Res. 23, 223-240, 1992
A;Title: Naturally occurring NS gene variants in an A;Reference number: A45575; MUID:92327829
A;Accession: A45575
                                                                                                                                                                                                                                                                                                                                   C;Species: influenza A virus
C;Date: 22-Apr-1993 #sequence_revision
C;Accession: A45575
                                                                                                                                                                                     A; Molecule type: genomic RNA
A; Residues: 1-230 < PER>
                                                                                                                                                                                                                                                                                                                                                                                 nonstructural protein NS1 - influenza A virus (strain A/Turkey/Wisconsin/68 [H5N9])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Map position: segment 8
C;Superfamily: influenza virus
C;Keywords: alternative splicir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nonstructural protein NS1 - influenza A virus (strain A/pintail/Alberta/358/79) c;Species: influenza A virus (c;Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 08-Apr-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: NSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: genomic RNA
A; Residues: 1-230 <TRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R; Treanor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Map position: segment 8
C;Superfamily: influenza virus nonstructural protein NS1
C;Keywords: alternative splicing; nonstructural protein
Query Match
Best Local Similarity 85.,
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A; Accession: E32663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Molecule type: genomic RNA
A;Residues: 1-230 <TRE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title:
                                                                                                                                                                                                                         Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Accession: G32663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      198 IQRFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          198 IORFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
nes 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ISRFAWG 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The B allele of the NS gene of avian influenza viruses, but not not number: A32662; MUID:89299445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            J.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Snyder, M.H.; London, W.T.; Murphy, B.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a virus nonstructural protein NS1
splicing; nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          73.5%;
85.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  73.5%;
85.7%;
                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                      Score 36; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB
Pred. No. 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 36; DB
Pred. No. 24;
                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                              22-Jul-1994 #text_change 19-May-2000
                                                         DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۲,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ۲,
                     ;;
                                                       Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1;
                                                                                                                                                                                                                                                                       avian influenza virus isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 230;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 230;
                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                             CTG for
                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the A allele,
                 0,
                                                                                                                                           residue 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
```

į

```
Search completed: October 18, Job time: 96 sec
                                                                                      В
                                                                                                                  Ş
                                                                                                                                                                                                                              C; Superfamily: replication initiation protein dnaP
                                                                                                                                                                                                                                                                                                                                             R;El-Karoui, M.; Ehrlich, D.; Gruss, A.
Proc. Natl. Acad. Sci. U.S.A. 95, 626-631, 1998
A;Title: Identification of the lactococcal exonuclease/recombinase and its modulation
A;Reference number: Z20817; MUID:98118563
A;Accession: T30305
                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
T30305
                                                                                                                                                                                                                                                         A; Gene: dnaA
                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U76424; NID:g2909712; PID:g2909713; PIDN:AAC12963.1
                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-272 <ELK>
                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                           C; Accession: T30305
                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Lactococcus lactis
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ş
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         dnaA protein - Lactococcus lactis (fragment)
                                                                                                                                                    Matches
                                                                                                                                                                    Query Match
Best Local
                                                                                 1 ISRFAWG 7 :|||:|| 86 VSRFSWG 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 198 IQRFAWG 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISRFAWG
                                                                                                                                                    Similarity 5; Conserv
                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7
                                                                                                                                                                  73.5%;
              2001, 16:52:11
                                                                                                                                                  2;
                                                                                                                                                                Score 36; DB
Pred. No. 28;
                                                                                                                                                Mismatches
                                                                                                                                                                                2
                                                                                                                                                0;
                                                                                                                                                                              Length 272;
                                                                                                                                               Indels
                                                                                                                                             0,:
                                                                                                                                             Gaps
                                                                                                                                           0
```